

1 / 39

1 DIVLTQSPAS LAVSLGQORAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL
 51 LIYRASNLLES GIPVRFSGTG SRTDFTLIID PVEADDVATY YCQOTNEDPY
 101 TFGGGTKLEI KGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SEVQLOQSGA
 151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK
 201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
 251 YWGOGTSVTV SS (SEQ ID NO:1)

FIG._1A

1 GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGGCTGTTT CCCTGGGCCA
 51 GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
 101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
 201 CGGTACTGGC TCTCGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
 351 TGGTGGTGGT AGCGGCGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
 451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
 501 TTTCAACATT AAGGACACCT ACATGCAC TG GGTGAAACAA CGCCCGGAAC
 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
 651 TAACACTGCT TACCTGCAGC TGACTTCC CT GACTAGCGAA GACACCGCGG
 701 TTTATTACTG CGCTCCGTTT GGCTACTA TG TCAGCGATTA CGCAATGGCC
 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGC (SEQ ID NO:3)

FIG._1B

263 TPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP
 301 HYYTFGKADI AANKPVTPQT LFELGSISK FTGVLGGDAI ARGEISLDDA
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
 451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM
 602 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:11)

FIG._1C

BEST AVAILABLE COPY

2 / 39

```

1  ACACCGGTGT CAGAAAAACA GCTGGCGGAG GTGGTCGCGA A'TACGATTAC
51  CCCGCTGATG AAAGCCCAGT CTGTTCCAGG CATGGCGGTG GCCGTTATTT
101 ATCAGGGAAA ACCGCACTAT TACACATTTG GCAAGGCCGA TATCGCGGCG
151 AATAAACCCG TTACGCCTCA GACCTGTTC GAGCTGGGT C'TATAAGTAA
201 AACCTTCACC GGCGTTTTAG GTGGGGATGC CATTGCTCGC GGTGAAATTT
251 CGCTGGACGA TGCGGTGACC AGATACTGGC CACAGCTGAC GGGCAAGCAG
301 TGGCAGGGTA TTCGTATGCT GGATCTCGCC ACCTACACCG CTGGCGGCCT
351 GCCGCTACAG GTACCGGATG AGGTCACGGA TAACGCCTCC CTGCTGCGCT
401 TTTATCAAAA CTGGCAGCCG CAGTGGAAGC CTGGCACAAC GCGTCTTTAC
451 GCCAACGCCA GCATCGGTCT TTTTGGTGCG CTGGCGGTCA AACCTTCTGG
501 CATGCCCTAT GAGCAGGCCA TGACGACGCG GGTCCTTAAG CCGCTCAAGC
551 TGGACCATAC CTGGATTAAC GTGCCGAAAG CGGAAGAGGC GCATTACGCC
601 TGGGGCTATC GTGACGGTAA AGCGGTGCGC GTTTCGCCGG GTATGCTGGA
651 TGCACAAGCC TATGGCGTGA AAACCAACGT GCAGGATATG GCGAACTGGG
701 TCATGGCAAA CATGGCGCCG GAGAACGTTG CTGATGCCTC ACTTAAGCAG
751 GGCATCGCGC TGGCGCAGTC GCGCTACTGG CGTATCGGGT CAATGTATCA
801 GGGTCTGGGC TGGGAGATGC TCAACTGGCC CGTGGAGGCC AACACGGTGG
851 TCGAGACGAG TTTTGGTAAT GTAGCACTGG CGCCGTTGCC CGTGGCAGAA
901 GTGAATCCAC CGGCTCCCCC GGTCAAAGCG TCCTGGGTCC ATAAAACGGG
951 CTCTACTGGC GGGTTTGGA GCTACGTGGC CTTTATTCCT GAAAAGCAGA
1001 TCGGTATTGT GATGCTCGCG AATACAAGCT ATCCGAACCC GGCACGCGTT
1051 GAGGCGGCAT ACCATATCCT CGAGGCGCTA CAG (SEQ ID NO:12)

```

FIG._1D

```

1  DIVLTQSPAS LAVSLGORAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL
51  LIYRASNL ES GIPVRFSGTG SRTDFTLIID PVEADDVATY YCQQTNEDPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKO RPEQGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
251 YWGQTSVTV SSTPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP
301 HYYTFGKADI AANKPVTPT LFE LGSISK FTGVLGGDAI ARGEISLDDA
351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
451 INVPKAE EAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWV MANM
501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
551 GNALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM
601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:2)

```

FIG._1E

3 / 39

```

1  GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGGCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTCGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGCGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CCGTGTGAGA
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
951 GCCTCAGACC CTGTTGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTGCTG GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCCTTTTA TCAAACTGG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:4)

```

FIG. 1F

```

1  DIVLTQSPAS LSVSLGORAT MSCRAGESVD IFGVGFLHWY OOKPGOPPKL
51  LIYRASNL ES GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQQTNE DPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEOGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAFP GYYVSDYAMA
251 YWGQGT SVTV SS (SEQ ID NO:5)

```

FIG. 2A

4 / 39

1 GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
 51 GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
 101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
 151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
 201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
 251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
 301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
 351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
 401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
 451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
 501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
 551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
 601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
 651 TAACACTGCT TACCTGCAGC TGA CTTCCT GACTAGCGAA GACACCGCGG
 701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
 751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGC (SEQ ID NO:6)

FIG._2B

262 TPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP
 301 HYYTFGKADI AANKPVTPQT LFELGSISK FTGVLGGDAI ARGEISLDDA
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
 451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM
 601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:13)

FIG._3

1 DIVLTQSPAS LSVSLGORAT MSCRAGESVD IFGVGFLHWY QOKPGOPPKL
51 LIYRASNLGS GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQQTNEPDPY
101 TFGGGTKLEI KGGGSGGGG SGGGSGGGG SGGGSGGGG SEVQLQOSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
251 YWGQTSVTV SSTPVSEKQL AEVVANTITP LMKAQSVPGM AVAVIYQGKP
 301 HYYTFGKADI AANKPVTPQT LFELGSISK FTGVLGGDAI ARGEISLDDA
 351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
 401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
 451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
 501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
 551 GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGSYVAF IPEKQIGIVM
 601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:7)

FIG._4A

5 / 39

```
1  GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCAC TG GTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA
801 AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGAAAG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
951 GCCTCAGACC CTGTTGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTGCTG GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCCTTTTA TCAAAACTGG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CCGTGGTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCAGCTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:9)
```

FIG. 4B

6 / 39

1 DIVLTQSPAS LSVSLGORAT MSCRAGESVD IFGVGFLHWY QOKPGQPPKL
51 LIYRASNLGS GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQOTNEDPY
101 TFGGGTKLEI KGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SEVQLQOSGA
151 ELVEPGASVK LSCTASGFNI KDTYMHVVKQ RPEQGLEWIG RIDPANGNSK
201 YVPKFQ GKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
251 YWGQGTSTVTV SSTPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP
301 HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA
351 VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
401 QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
451 INVPKAEAAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
501 APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
551 GNVALLPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM
601 LANTSYPNPA RVEAAYHILE ALQ (SEQ ID NO:8)

FIG. 4C

7 / 39

```
1  GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
101 TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAAC TG
151 CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
201 CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
251 CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
301 ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
351 TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
401 GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
451 GAGCTCGTTG AACC GGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
501 TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
551 AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
601 TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
651 TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
701 TTTATTACTG CGCTCCGTTT GGCTACTATG TCAGCGATTA CGCAATGGCC
751 TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA
801 AAAACAGCTG GCGGAGGTGG TCGGAATAC GATTACCCCG CTGATGGCGG
851 CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
901 CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACC CGTTAC
951 GCCTCAGACC CTGTTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001 TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTTCGCT GGACGATGCG
1051 GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG
1101 TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151 CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG
1201 CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251 CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301 AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351 ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401 CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451 GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501 GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551 GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601 AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT
1651 GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701 TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751 TTGGCGCGTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801 CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851 TATCCTCGAG GCGCTACAG (SEQ ID NO:10)
```

FIG. 4D

8 / 39

1	AGGAATTATC	ATATGAAATA	CCTGCTGCCG	ACCGCTGCTG	CTGGTCTGCT
51	GCTCCTCGCT	GCCCAGCCGG	CCATGGCCGA	CATCGTCCTG	ACCCAGAGCC
101	CGGCAAGCCT	GTCTGTTTCC	CTGGGCCAGC	GTGCCACTAT	GTCCTGCAGA
151	GCGGGTGAGT	CTGTTGACAT	TTTCGGTGTC	GGTTTTCTGC	ACTGGTACCA
201	ACAGAAACCG	GGTCAGCCGC	CAAAACTGCT	GATCTATCGT	GCTTCTAACC
251	TGGAGTCCGG	CATCCCAGTA	CGTTTCTCCG	GTACTGGCTC	TGGTACTGAT
301	TTTACCCTGA	TTATCGACCC	GGTGGAAGCA	GACGATGTTG	CCACCTACTA
351	TTGCCAGCAG	ACCAACGAGG	ATCCGTACAC	CTTCGGTGGC	GGTACTAAAC
401	TGGAGATCAA	AGGCGGTGGT	GGTTCTGGTG	GTGGTGGTAG	CGGTGGCGGT
451	GGTAGCGGTG	GCGGTGGCAG	CGGTGGTGGT	GGCTCTGGTG	GCGGTGGCTC
501	TGAAGTGCAG	CTGCAGCAGT	CCGGTGCGGA	GCTCGTTGAA	CCGGGCGCTT
551	CTGTGAAACT	GTCTTGCACT	GCATCTGGTT	TCAACATTAA	GGACACCTAC
601	ATGCACTGGG	TGAAACAACG	CCCGGAACAG	GGTCTGGAGT	GGATCGGTCTG
651	CATCGATCCG	GCTAACGGTA	ACAGCAAATA	CGTGCCAAAA	TTCCAGGGTA
701	AAGCAACCAT	CACTGCTGAT	ACCTCCTCTA	ACACTGCTTA	CCTGCAGCTG
751	ACTTCCCTGA	CTAGCGAAGA	CACCGCGGTT	TATTACTGCG	CTCCGTTCCG
801	CTACTATGTC	AGCGATTACG	CAATGGCCTA	CTGGGGTCAG	GGCACCTCTG
851	TTACCGTTTC	TAGCACACCG	GTGTCAGAAA	AACAGCTGGC	GGAGGTGGTC
901	GCGAATACGA	TTACCCCGCT	GATGGCGGCC	CAGTCTGTTC	CAGGCATGGC
951	GGTGGCCGTT	ATTTATCAGG	GAAAACCGCA	CTATTACACA	TTTGGCAAGG
1001	CCGATATCGC	GGCGAATAAA	CCCGTTACGC	CTCAGACCCT	GTTTCGAGCTG
1051	GGTTCCTATA	GTAAAACCTT	CACCGGCGTT	TTAGGTGGGG	ATGCCATTGC
1101	TCGCGGTGAA	ATTTTCGCTG	ACGATGCGGT	GACCAGATAC	TGGCCACAGC
1151	TGACGGGCAA	GCAGTGGCAG	GGTATTCGTA	TGCTGGATCT	CGCCACCTAC
1201	ACCGCTGGCG	GCCTGCCGCT	ACAGGTACCG	GATGAGGTCA	CGGATAACGC
1251	CTCCCTGCTG	CGCTTTTATC	AAAACCTGGCA	GCCGCAGTGG	AAGCCTGGCA
1301	CAACGCGTCT	TTACGCCAAC	GCCAGCATCG	GTCTTTTGG	TGCGCTGGCG
1351	GTCAAACCTT	CTGGCATGCC	CTATGAGCAG	GCCATGACGA	CGCGGGTCCT
1401	TAAGCCGCTC	AAGCTGGACC	ATACCTGGAT	TAACGTGCCG	AAAGCGGAAG
1451	AGGCGCATT	CGCCTGGGGC	TATCGTGACG	GTAAAGCGGT	GCGCGTTTCG
1501	CCGGGTATGC	TGGATGCACA	AGCCTATGGC	GTGAAAACCA	ACGTGCAGGA
1551	TATGGCGAAC	TGGGTCATGG	CAAACATGGC	GCCGGAGAAC	GTTGCTGATG
1601	CCTCACTTAA	GCAGGGCATC	GCGCTGGCGC	AGTCGCGCTA	CTGGCGTATC
1651	GGGTCAATGT	ATCAGGGTCT	GGGCTGGGAG	ATGCTCAACT	GGCCCGTGGA
1701	GGCCAACACG	GTGGTCGAGA	CGAGTTTGG	TAATGTAGCA	CTGGCGCCGT
1751	TGCCCGTGCC	AGAAGTGAAT	CCACCGGCTC	CCCCGGTCAA	AGCGTCCTGG
1801	GTCCATAAAA	CGGGCTCTAC	TGGCGGGTTT	GGCGCGTACG	TGGCCTTTAT
1851	TCCTGAAAAG	CAGATCGGTA	TTGTGATGCT	CGCGAATACA	AGCTATCCGA
1901	ACCCGGCACG	CGTTGAGGCG	GCATACCATA	TCCTCGAGGC	GCTACAGTAG
1951	GAATTCGAGC	TCCGTCGACA	AGCTTGCGGC	CGCACTCGAG	ATCAAACGGG
2001	CTAGCCAGCC	AGAACTCGCC	CCGGAAGACC	CCGAGGATGT	CGAGCACCAC
2051	CACCACCACC	ACTGAGATCC	GGCTGCTAAC	AAAGCCCGAA	AGGAAGCTGA
2101	GTTGGCTGCT	GCCACCGCTG	AGCAATAACT	AGCATAACCC	CTTGGGGCCT
2151	CTAAACGGGT	CTTGAGGGGT	TTTTTGCTGA	AAGGAGGAAC	TATATCCGGA
2201	TTGGCGAATG	GGACGCGCCC	TGTAGCGGCG	CATTAAGCGC	GGCGGGTGTG
2251	GTGGTTACGC	GCAGCGTGAC	CGCTACACTT	GCCAGCGCCC	TAGCGCCCGC
2301	TCCTTTCGCT	TTCTTCCCTT	CCTTCTCGC	CACGTTCCGC	GGCTTTCGCC

FIG. 4E-1

SUBSTITUTE SHEET (RULE 26)

9 / 39

2351	GTCAAGCTCT	AAATCGGGGG	CTCCCTTTAG	GGTTCCGATT	TAGTGCTTTA
2401	CGGCACCTCG	ACCCCAAAA	ACTTGATTAG	GGTGATGGTT	CACGTAGTGG
2451	GCCATCGCCC	TGATAGACGG	TTTTTCGCCC	TTTGACGTTG	GAGTCACGT
2501	TCTTTAATAG	TGGACTCTTG	TTCCAAACTG	GAACAACACT	CAACCCTATC
2551	TCGGTCTATT	CTTTTGATTT	ATAAGGGATT	TTGCCGATTT	CGGCC TATTG
2601	GTTAAAAAAT	GAGCTGATTT	AACAAAAAAT	TAACGCGAAT	TTTAA CAAAA
2651	TATTAACGCT	TACAATTTCC	TGATGCGGTA	TTTTCTCCTT	ACGCA TCTGT
2701	GCGGTATTTT	ACACCGCATA	TGGTGCACCT	TCAGTACAAT	CTGCTCTGAT
2751	GCCGCATAGT	TAAGCCAGCC	CCGACACCCG	CCAACACCCG	CTGAC GCGCC
2801	CTGACGGGCT	TGTCTGCTCC	CGGCATCCGC	TTACAGACAA	GCTGTGACCG
2851	TCTCCGGGAG	CTGCATGTGT	CAGAGGTTTT	CACCGTCATC	ACCGA AACGC
2901	GCGAGACGAA	AGGGCCTCGT	GATACGCCTA	TTTTTATAGG	TTAATGTCAT
2951	GATAATAATG	GTTTCTTAGA	CGTCAGGTGG	CACTTTTCGG	GGAAATGTGC
3001	GCGGAACCCC	TATTTGT TTA	TTTTTCTAAA	TACATTCAAA	TATGTATCCG
3051	CTCATGAGAC	AATAACCTTG	TGGCAGCATC	ACCCGACGCA	CTTTGCGCCG
3101	AATAAATACC	TGTGACGGAA	GATCACTTCG	CAGAATAAAT	AAATCCTGGT
3151	GTCCCTGTTG	ATACCGGGAA	GCCCTGGGCC	AACTTTTGGC	GAAATGAGA
3201	CGTTGATCGG	CACGTAAGAG	GTTCCAACCT	TCACCATAAT	GAAATAAGAT
3251	CACTACCGGG	CGTATTT TTT	GAGTTATCGA	GATTTTCAGG	AGCTAAGGAA
3301	GCTAAAATGG	AGAAAAAAT	CAC TGGATAT	ACCACCGTTG	ATATATCCCA
3351	ATGGCATCGT	AAAGAACATT	TTGAGGCATT	TCAGTCAGTT	GCTCAATGTA
3401	CCTATAACCA	GACCGTTCAG	CTGGATATTA	CGGCCTTTTT	AAAGACCGTA
3451	AAGAAAAATA	AGCACAAGTT	TTATCCGGCC	TTTATTCACA	TTCTTGCCCG
3501	CCTGATGAAT	GCTCATCCGG	AATTCCGTAT	GGCAATGAAA	GACG GTGAGC
3551	TGGTGATATG	GGATAGTGTT	CACCCTTGTT	ACACCGTTTT	CCATGAGCAA
3601	ACTGAAACGT	TTTCATCGCT	CTGGAGTGAA	TACCACGACG	ATTTCCGGCA
3651	GTTTCTACAC	ATATATTCGC	AAGATGTGGC	GTGTTACGGT	GAAAACCTGG
3701	CCTATTTCCC	TAAAGGGTTT	ATTGAGAATA	TGTTTTTCGT	CTCAGCCAAT
3751	CCCTGGGTGA	GTTTCACCAG	TTTTGATTTA	AACGTGGCCA	ATATGGACAA
3801	CTTCTTCGCC	CCCGTTT TCA	CGATGGGCAA	ATATTATACG	CAAGCGGACA
3851	AGGTGCTGAT	GCCGCTGGCG	ATTCAGGTTC	ATCATGCCGT	CTGTGATGGC
3901	TTCCATGTCG	GCAGAA TGCT	TAATGAATTA	CAACAGTACT	GCGATGAGTG
3951	GCAGGGCGGG	GCGTAAAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA
4001	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	CATATATACT	TTAGATTGAT
4051	TTAAAACCTC	ATTTTTAATT	TAAAAGGATC	TAGGTGAAGA	TCCTTTTTTGA
4101	TAATCTCATG	ACCAAAATCC	CTTAACGTGA	GTTTTTCGTT	CAC T GAGCGT
4151	CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTTCTG
4201	CGCGTAATCT	GCTGCTTGCA	AACAAAAAAA	CCACCGCTAC	CAGCGGTGGT
4251	TTGTTTGCCG	GATCAAGAGC	TACCAACTCT	TTTTCCGAAG	GTA ACTGGCT
4301	TCAGCAGAGC	GCAGATACCA	AATACTGTTC	TTCTAGTGTA	GCCGTAGTTA
4351	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC	TCGCTCTGCT
4401	AATCCTGTTA	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG	TGTCTTACCG
4451	GGTTGGACTC	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA
4501	ACGGGGGGTT	CGTGCA CACA	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA
4551	ACTGAGATAC	CTACAGCGTG	AGCTATGAGA	AAGCGCCACG	CTTCCCGAAG
4601	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	GCAGGGTCGG	AACAGGAGAG
4651	CGCACGAGGG	AGCTTC CAGG	GGGAAACGCC	TGGTATCTTT	ATAGTCCTGT

FIG. 4E-2

SUBSTITUTE SHEET (RULE 26)

10/39

4701 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG
4751 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC
4801 CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC
4851 TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC
4901 GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA
4951 GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA
5001 ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA
5051 ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
5101 TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
5151 TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTA TTTAGGTGAC
5201 ACTATAGAAT ACTCAAGCTT TCTAGATTAA GG

FIG._4E-3

11 / 39

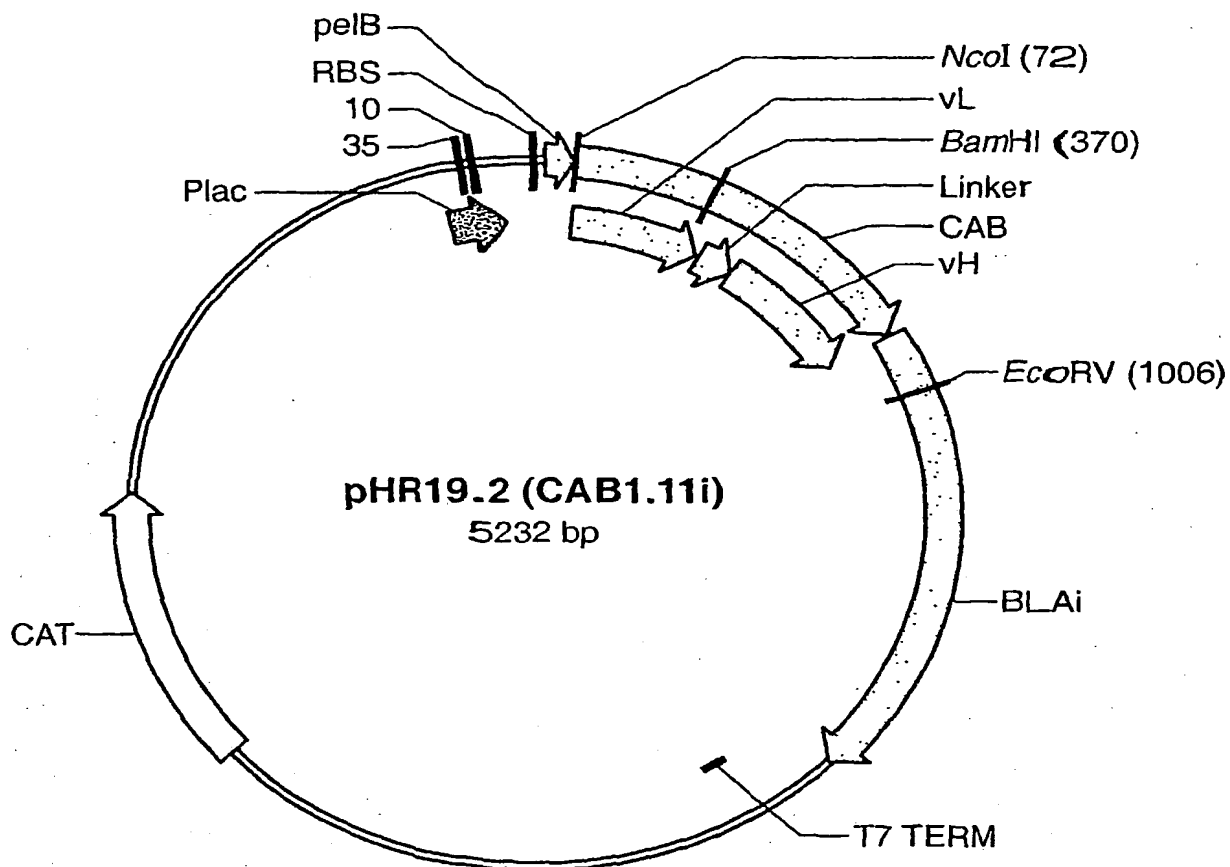


FIG._5

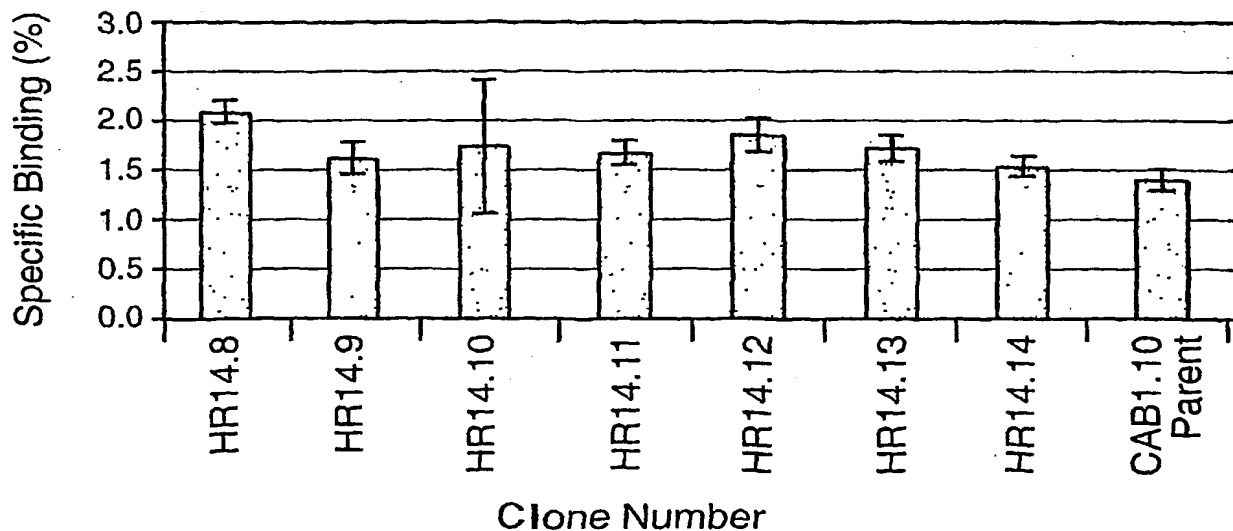
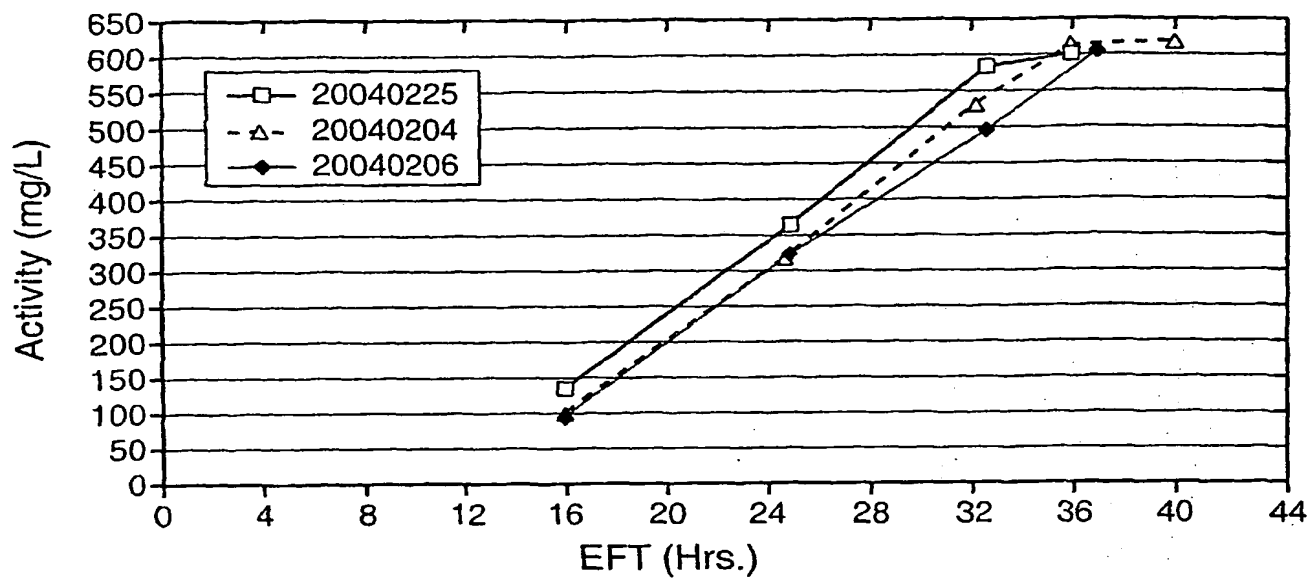
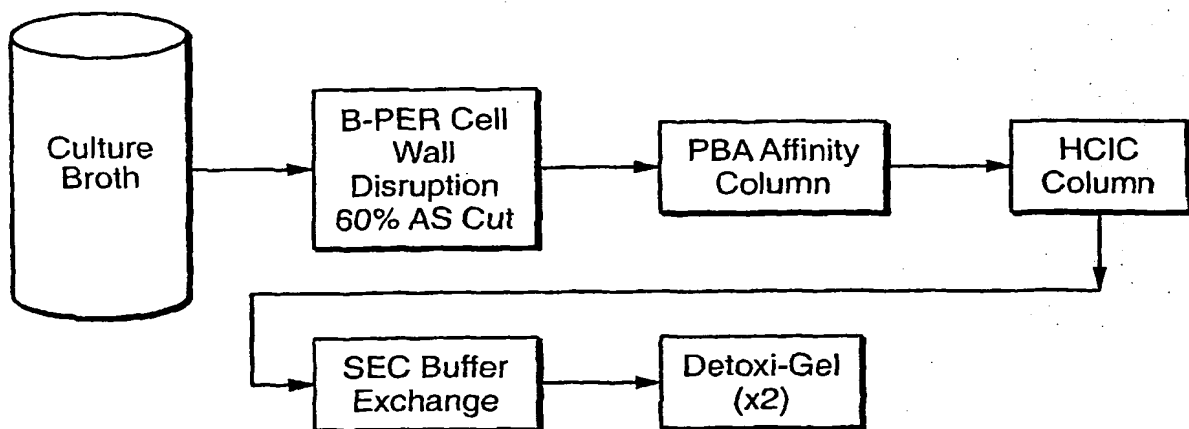


FIG._6

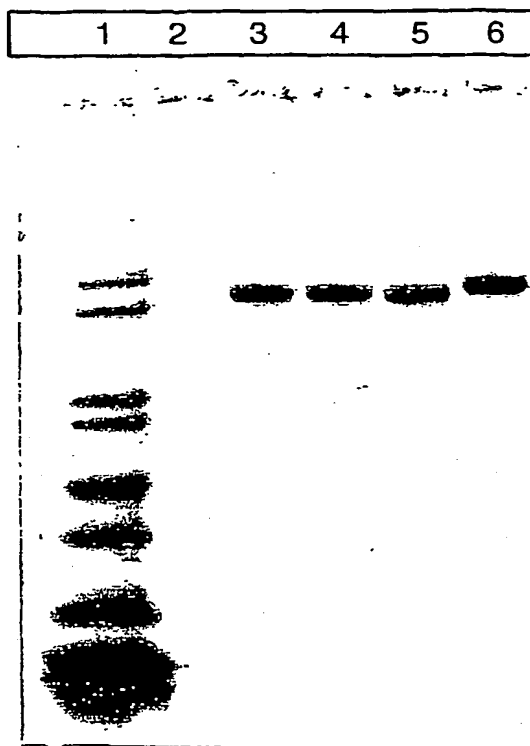
12 / 39

ADEPT 14L; EB101.1/pHR19.2, CAB1.11i

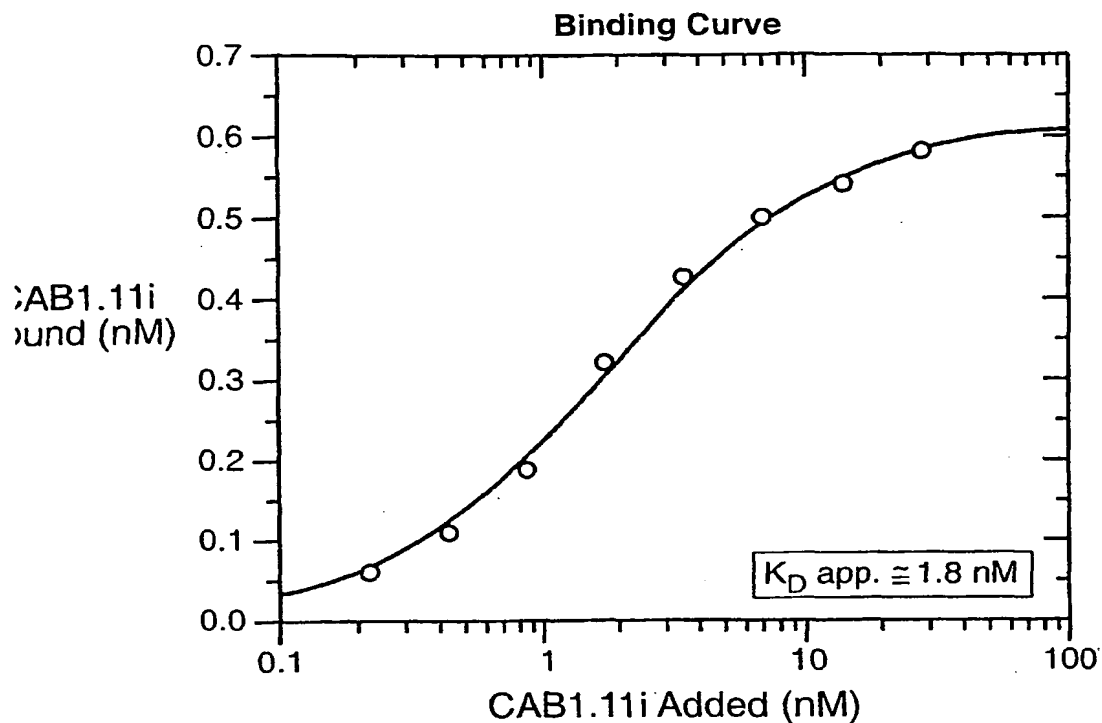
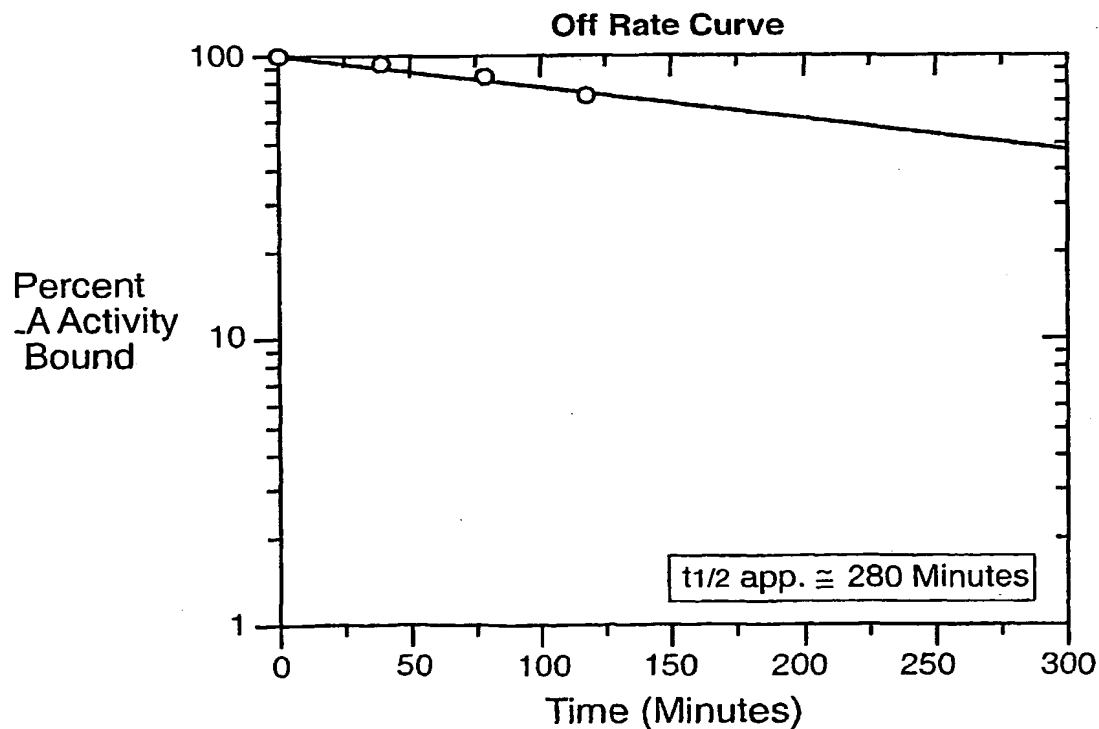
**FIG. 7****FIG. 8**

13 / 39

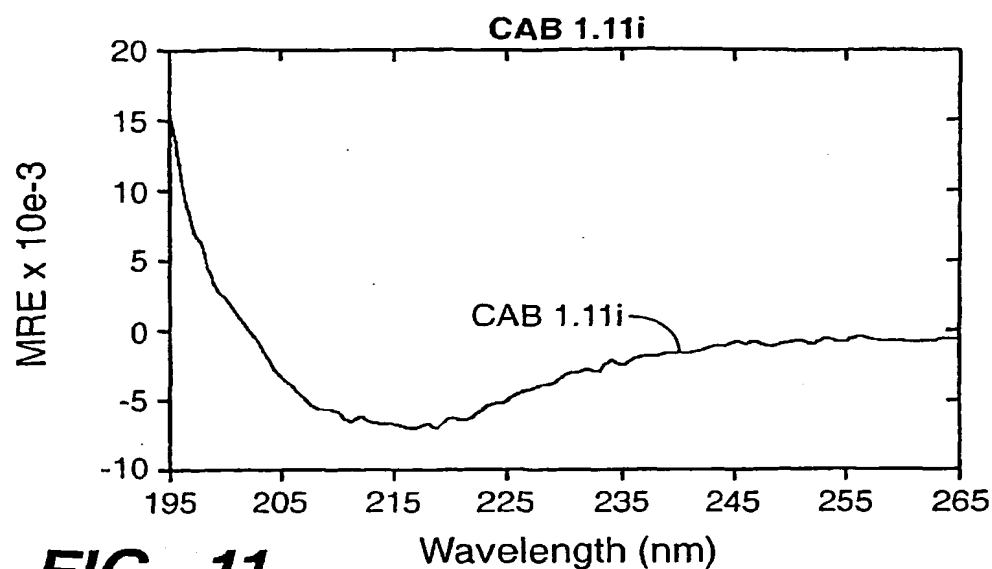
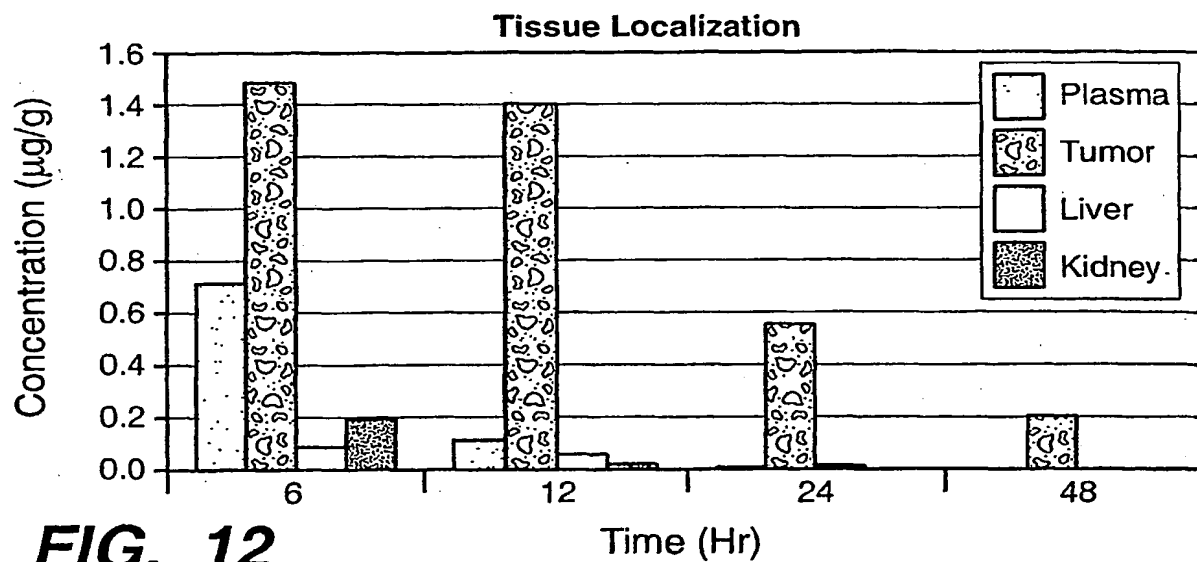
Lane 1: Molecular Weight Standard; Lanes 3-5: Unrelated Proteins; Lane 6: CAB1.11i.

**FIG. 9**

14 / 39

**FIG. 10A****FIG. 10B**

15 / 39

**FIG. 11****FIG. 12**

16 / 39

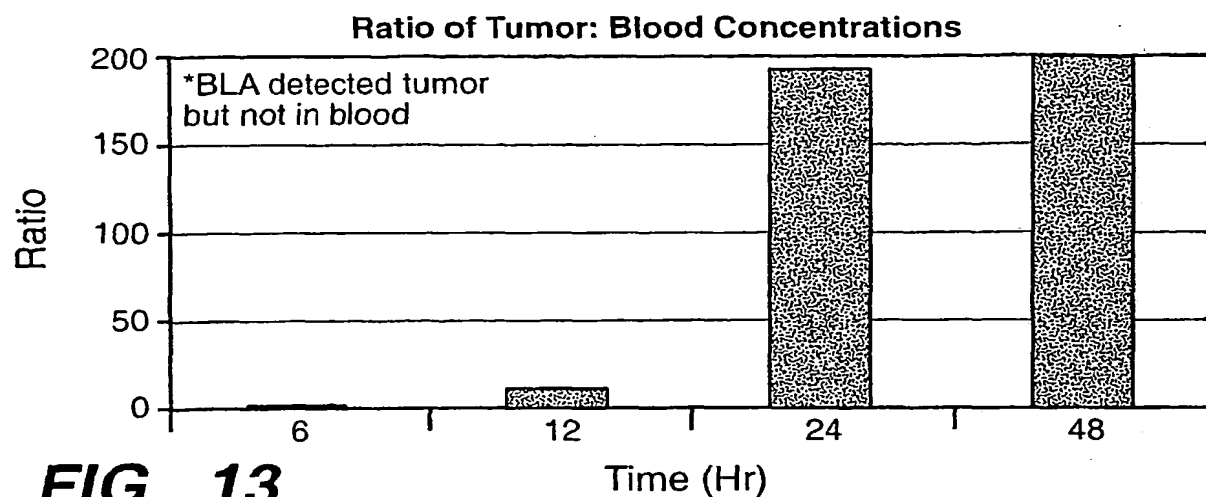
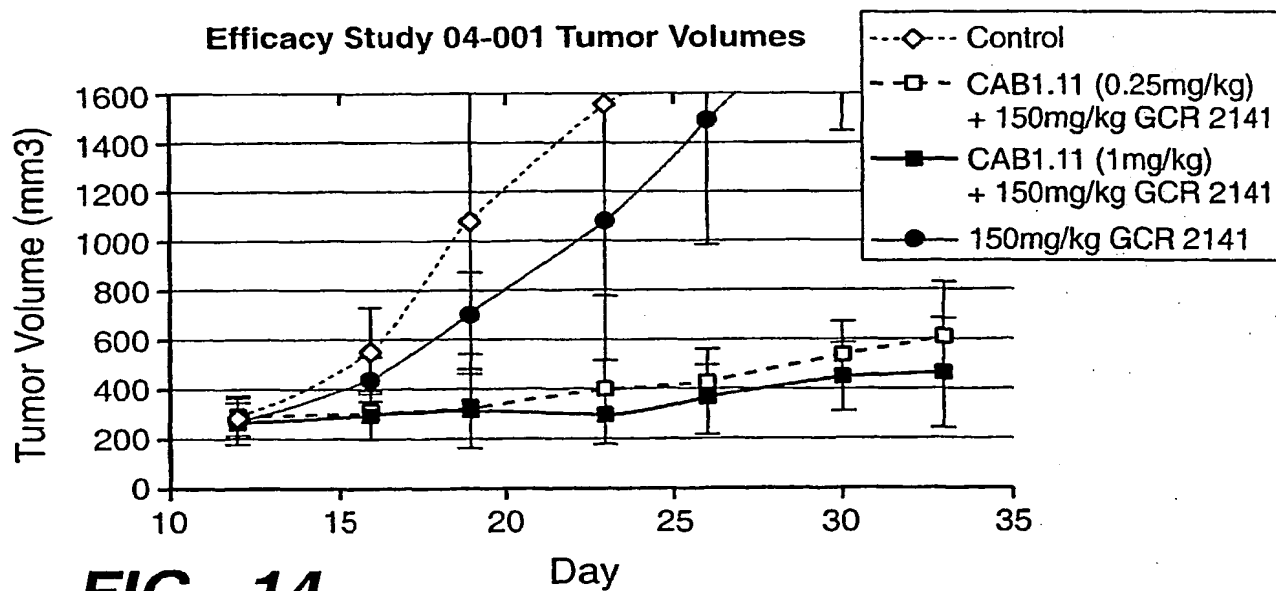
**FIG. 13****FIG. 14**

FIG. 15A

Case ID	ASM	Sample ID	Sample Pathology
<u>CI0000000255</u>	DF5	FR00005C7B	Adenocarcinoma of lung
<u>CI0000005496</u>	FF5	FR5B337147	Adenocarcinoma of lung
<u>CI0000011577</u>	FF1	FR5B34059F	Adenocarcinoma of lung
<u>CI7000000241</u>	AF4	FR00033A78	Adenocarcinoma of lung
<u>CI0000007518</u>	AF5	FR0001FD15	Carcinoma of lung, squamous cell
<u>CI0000008475</u>	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
<u>CI0000015252</u>	FF2	FR5B342166	Adenocarcinoma of colon

FIG. 15B

Case Diagnosis	Tissue of Origin/Site of Finding	H/E
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	<u>4X</u> <u>20X</u>
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	<u>4X</u> <u>20X</u>
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	<u>4X</u> <u>20X</u>

Anti-Human Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029758</u>	Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029756</u>
	Immunogenicity: Tumor (15%, Variable to 3+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975B</u>
	Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977F</u>
	Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002978B</u>
	Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975F</u>
Immunogenicity: Tumor (98%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (2+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002976A</u>	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029768</u> Normal liver parenchyma shows positive staining (1+)
	Immunogenicity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029783</u>

FIG. 15D

CAB/GCR5517 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 3+ Cyto) Necrosis (Variable to 2+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029757</u>	Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029753</u>
Immunogenicity: Tumor (40%, Variable to 3+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975C</u>	Immunogenicity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029759</u>
Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029780</u>	Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002977D</u>
Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002978C</u>	Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029789</u>
Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029760</u>	Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF0002975D</u>
Immunogenicity: Tumor (98%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (2+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029769</u>	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029765</u> Normal liver parenchyma shows positive staining (1+)
Immunogenicity: Tumor (85%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029784</u>	Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <u>4x</u> <u>20x</u> <u>SF00029781</u>

FIG. 15E

CAB/GCR8886 (0.196ug/ml)	No Antibody Control (Prediluted)
Immunogenicity: Tumor (100%, Variable to 3+ Cyto) Mixed inflammatory cells (Variable to 1+ Cyto) Specificity: High <div> <div>4x</div> <div>SF00029754</div> <div>20x</div> </div>	Immunogenicity: N/A Specificity: Unknown <div>SF00029755</div>
Immunogenicity: Tumor (10%, Variable to 2+ Cyto) Intra-alveolar macrophages (Variable to 2+ Cyto) Mixed inflammatory cells (Variable to 2+ Cyto) Specificity: High <div> <div>4x</div> <div>SF0002975A</div> <div>20x</div> </div>	
Immunogenicity: Tumor (100%, 2+ Cyto) Cellular stroma (1+ Cyto) Chronic inflammatory cells (Variable to 1+ Cyto) Specificity: High <div> <div>4x</div> <div>SF0002977E</div> <div>20x</div> </div>	
Immunogenicity: Tumor (75%, Variable to 3+ Cyto) Cellular stroma (Variable to 2+ Cyto) Necrosis (Variable to 2+ EC) Intra-alveolar macrophages (Variable to 2+ Cyto) Specificity: High <div> <div>4x</div> <div>SF0002978A</div> <div>20x</div> </div>	
Immunogenicity: Tumor (100%, 3+ Cyto) Fibrotic stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <div> <div>4x</div> <div>SF0002975E</div> <div>20x</div> </div>	
Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Normal liver parenchyma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High <div> <div>4x</div> <div>SF00029766</div> <div>20x</div> </div> Normal liver parenchyma shows positive staining (1+)	Immunogenicity: N/A Specificity: Unknown <div>SF00029767</div>
Immunogenicity: Tumor (95%, Variable to 3+ Mem, Variable to 3+ Cyto) Cellular stroma (1+ Cyto) Normal muscle (Variable to 2+ Cyto) Specificity: High <div> <div>4x</div> <div>SF00029782</div> <div>20x</div> </div>	

22 / 39			
<u>CI0000017970</u>	HF1	FR65EE7B3D	Adenocarcinoma of colon
<u>CI0000010013</u>	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
<u>CI0000009651</u>	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
<u>CI0000008690</u>	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
<u>CI0000007678</u>	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
<u>CI0000009736</u>	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 15F

23 / 39

Adenocarcinoma of colon Grade: AJCC G3: Moderately differentiated Stage: IIIC	Colon/Colon	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	<u>4X</u> <u>20X</u>
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	<u>4X</u> <u>20X</u>

FIG. 15G

24 / 39

	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029787</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002977C</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002977A</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029771</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF0002976D</u></p>
	<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029763</u></p>
	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u></p> <p><u>SF00029775</u></p>

FIG. 15H

25 / 39

<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029788</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029785</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002977B</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029777</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029772</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029770</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976E</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976B</u></p>
<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029764</u></p>	<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029761</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029776</u></p>	<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Fibrotic stroma (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029773</u></p>

FIG. 15I

26 / 39

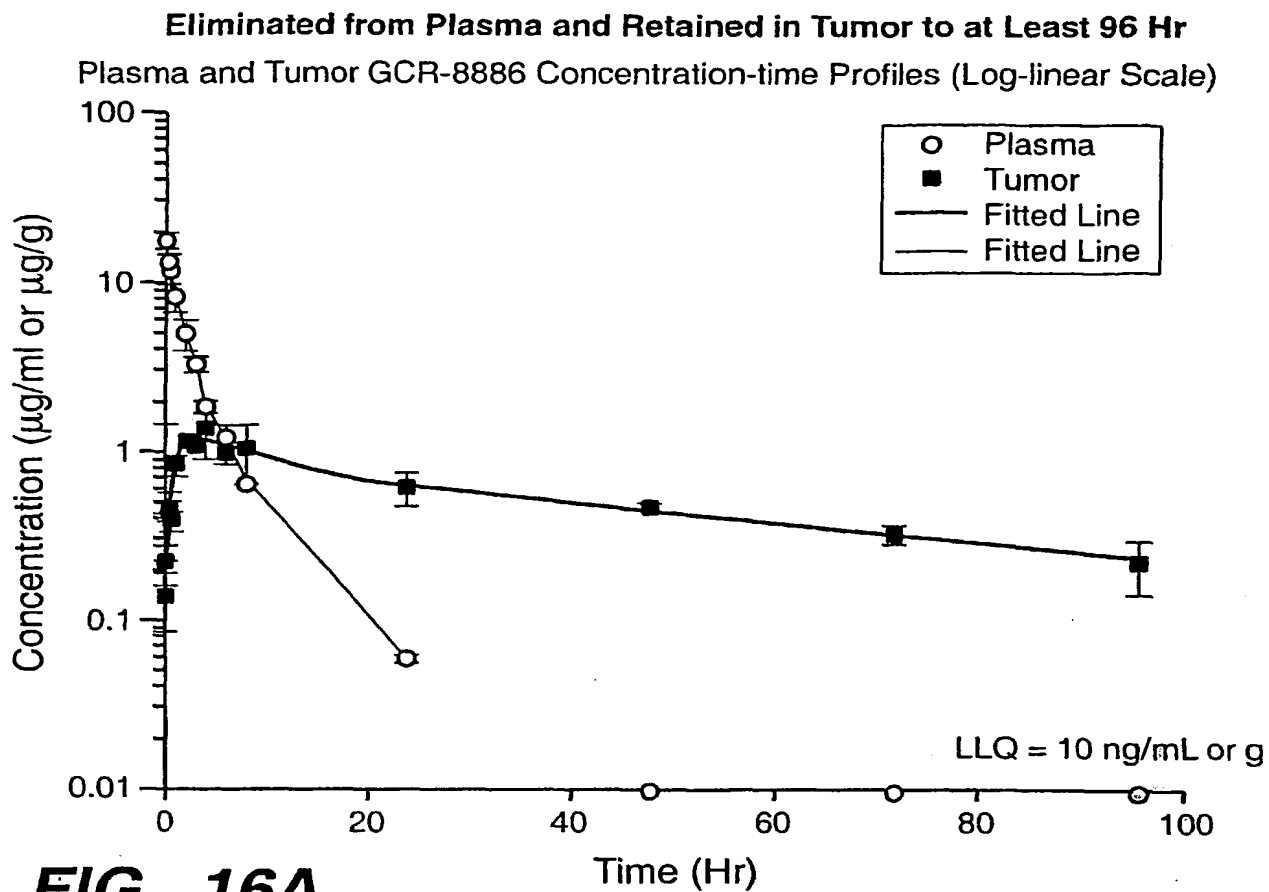
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Cellular stroma (1+ Cyto) Necrosis (Variable to 3+ EC) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029786</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Fibroadipose tissue (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029778</u></p>	<p>Immunogenicity: N/A Specificity: N/A</p> <p><u>SF00029779</u></p>
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Desmoplastic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976F</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Myxoid stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF0002976C</u></p>	
<p>Immunogenicity: Tumor (85%, Variable to 3+ Cyto) Cellular stroma (Variable to 1+ Cyto) Chronic pancreatitis (Variable to 1+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029762</u></p>	
<p>Immunogenicity: Tumor (100%, 3+ Cyto) Chronic pancreatitis (Variable to 2+ Cyto) Fibrotic stroma (Variable to 2+ Cyto) Specificity: High</p> <p><u>4x</u> <u>20x</u> <u>SF00029774</u></p>	

FIG._15J

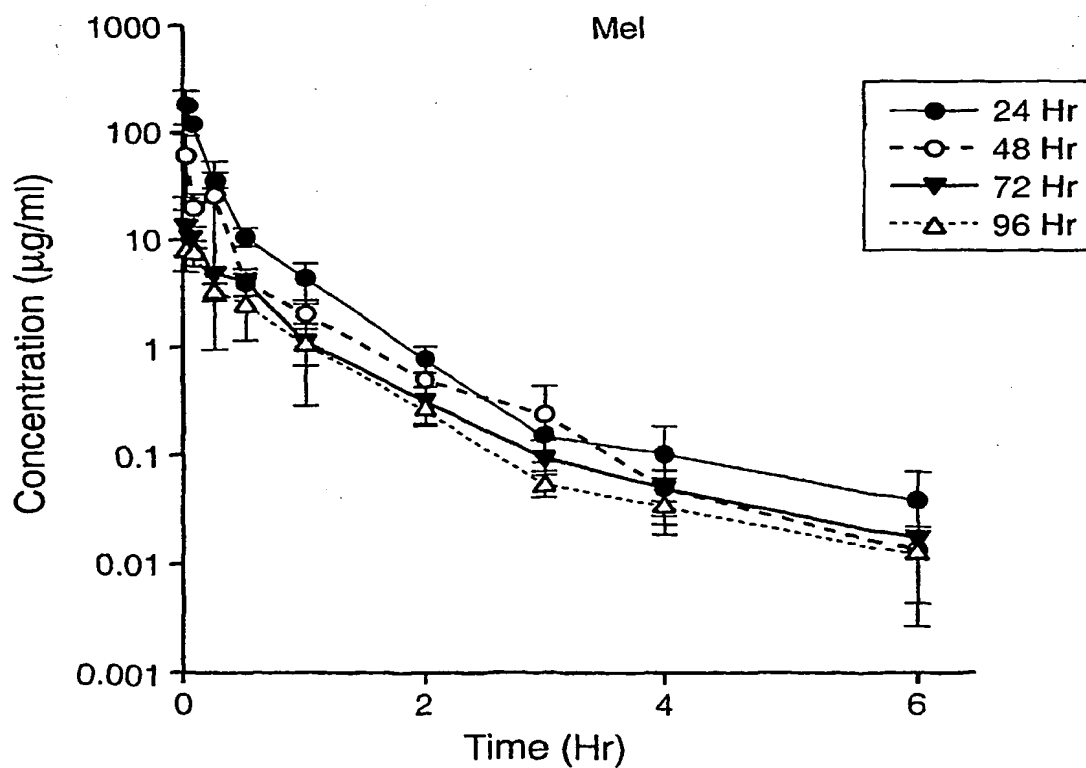
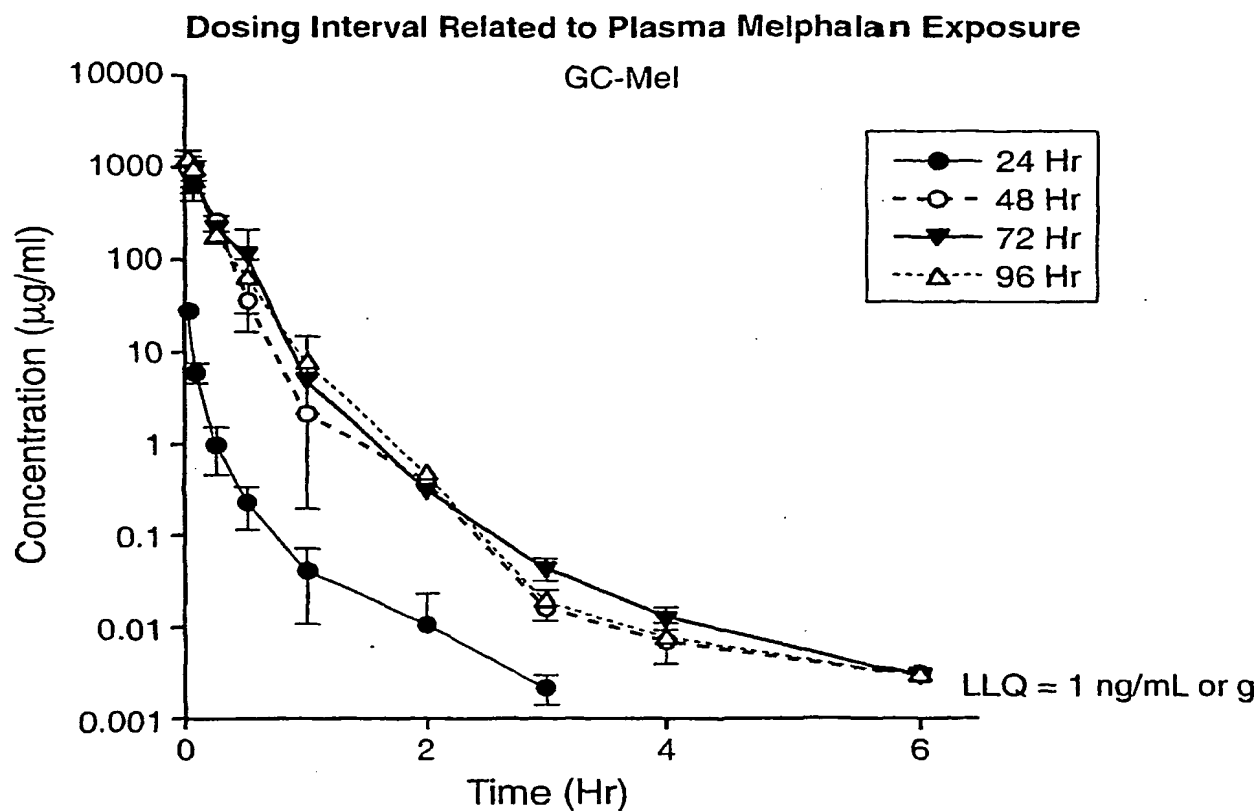
FIG._15A	FIG._15B	FIG._15C	FIG._15D	FIG._15E
FIG._15F	FIG._15G	FIG._15H	FIG._15I	FIG._15J

FIG._15

27 / 39

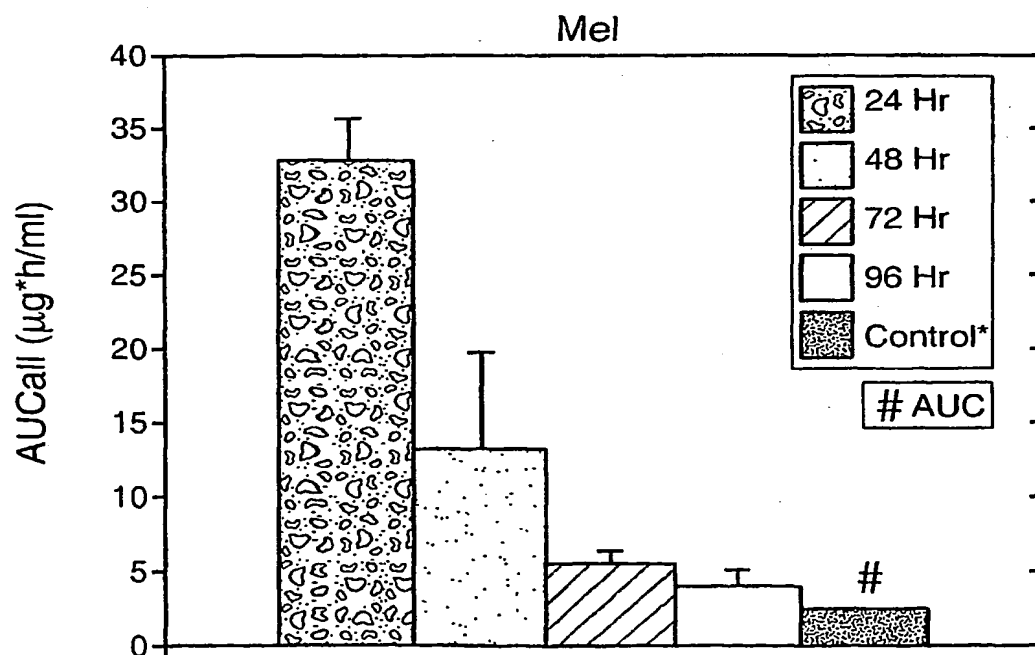
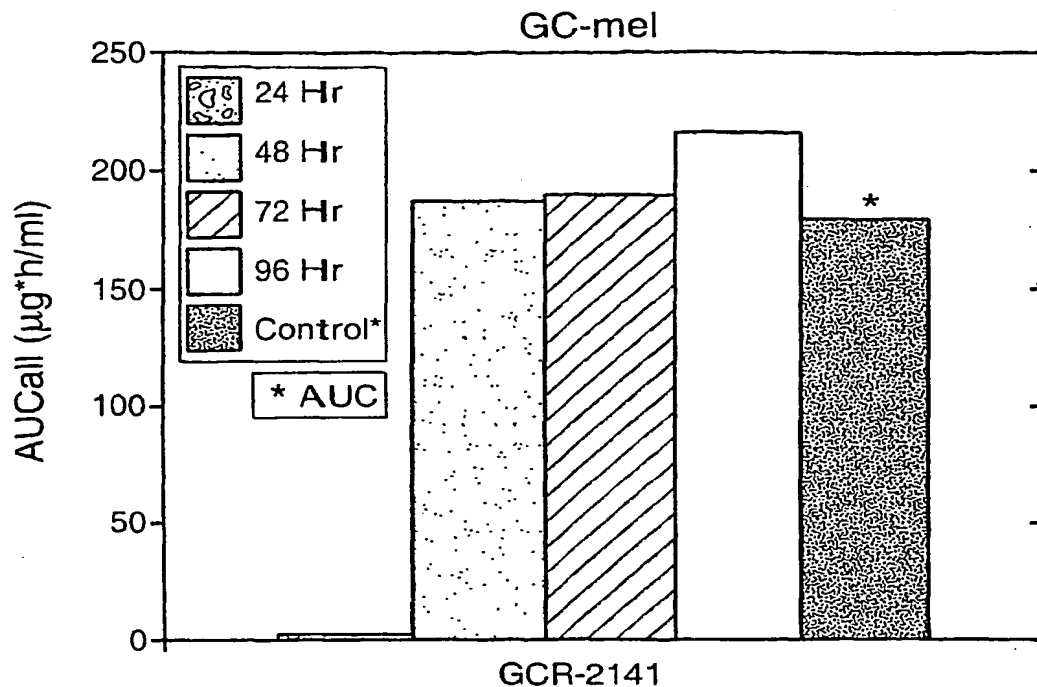
**FIG. 16A**

28 / 39

**FIG. 16B-1**

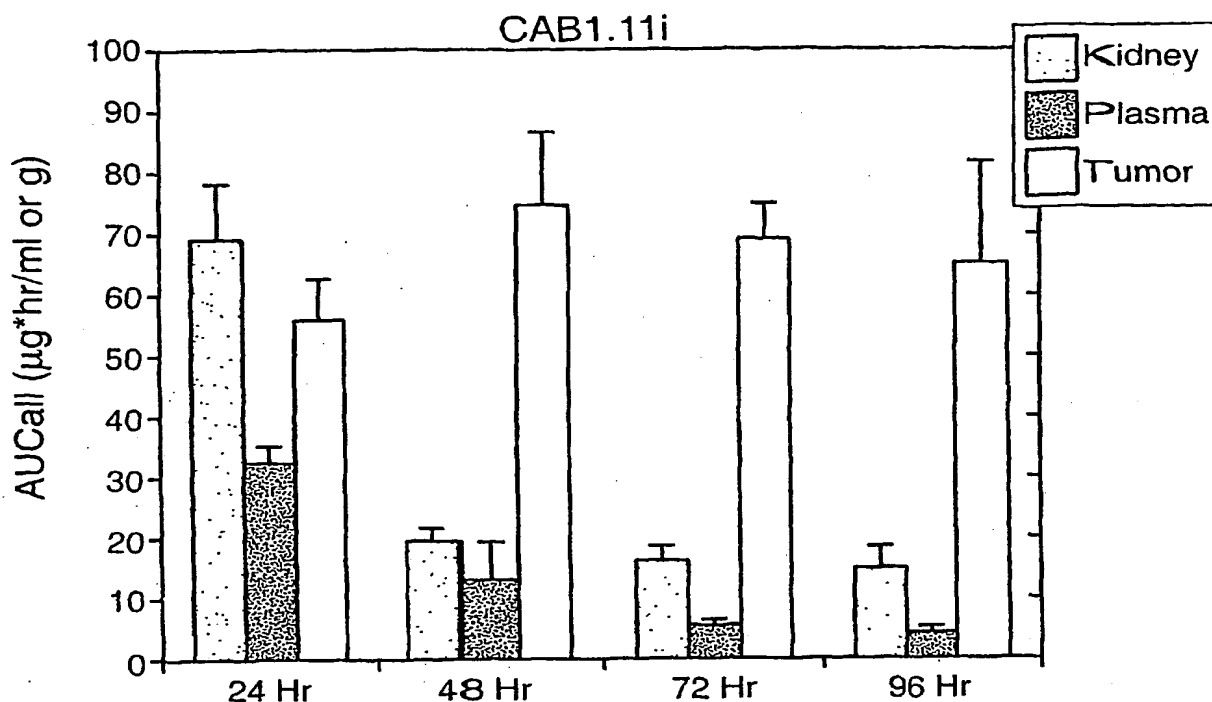
29 / 39

Dosing Interval Related to Plasma Melphalan Exposure

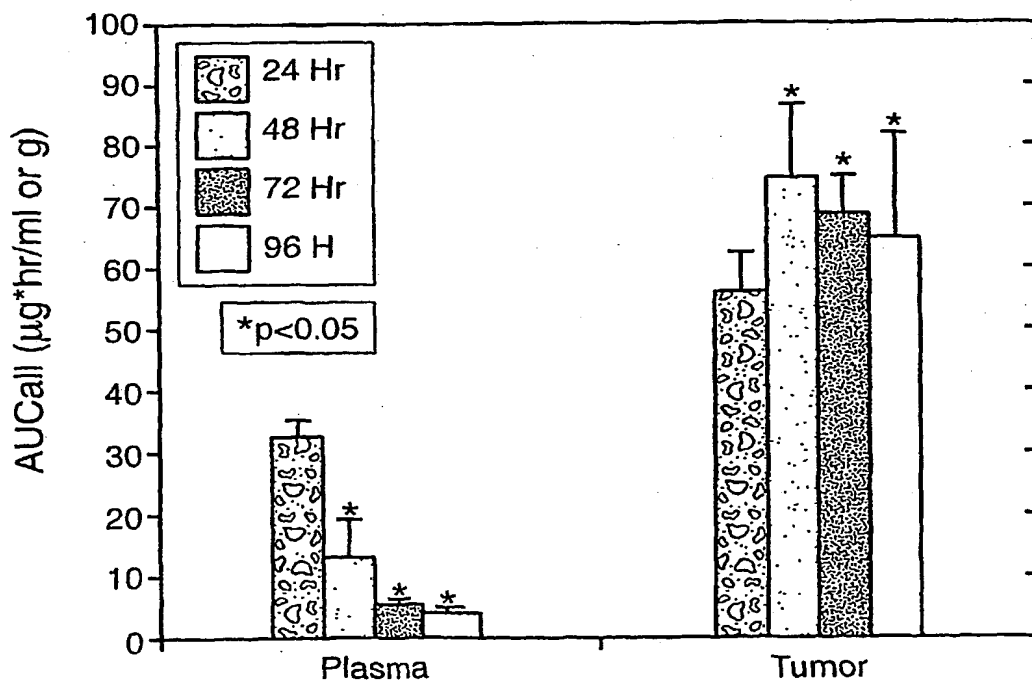
**FIG. 16B-2**

30 / 39

Plasma and Kidney Exposure to is Decreased with Increased Interval Between GCR CAB1.11i and GCR GC-mel Administration

**FIG. 17**

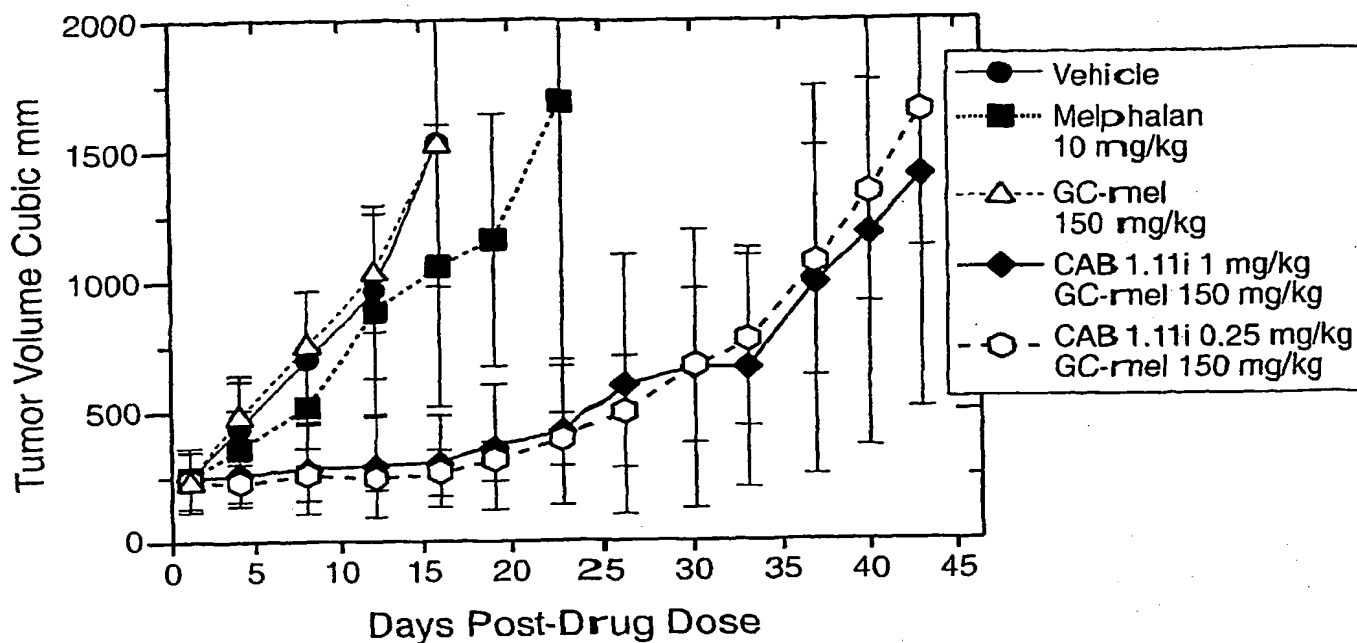
Efficacious Tumor Melphalan Exposures Achieved at Each Time Interval While Systemic Melphalan Exposure Decreased



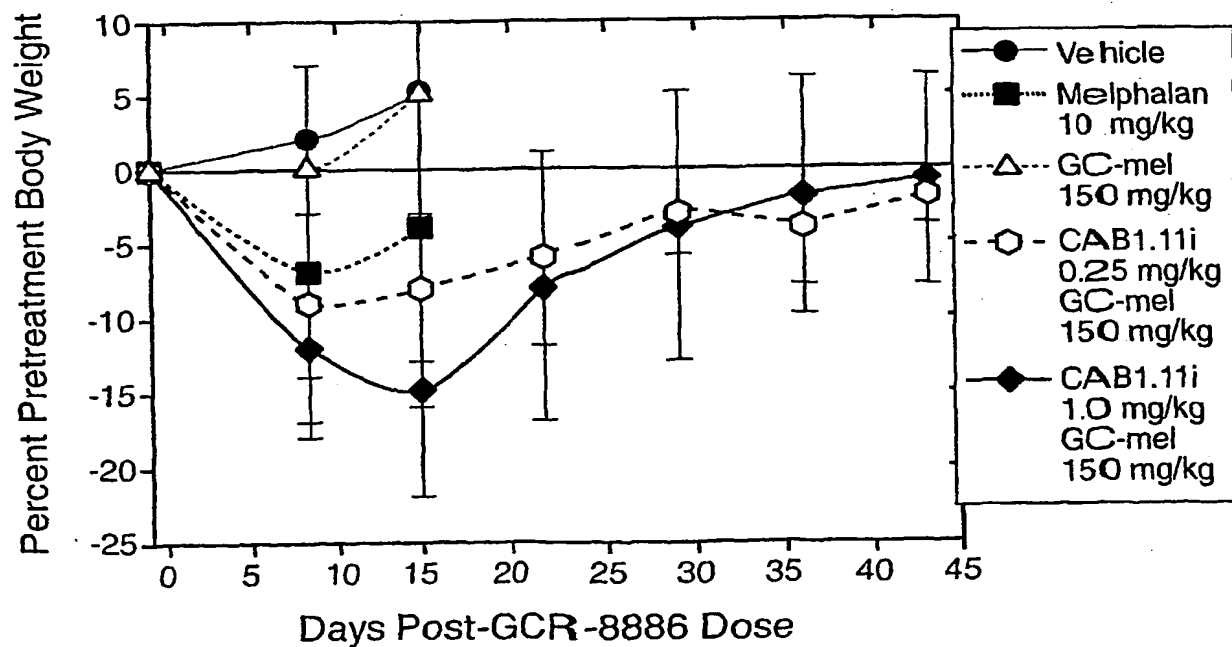
• Efficacy demonstrated at 24 hr interval in TLS174T xenograft mouse model

FIG. 18

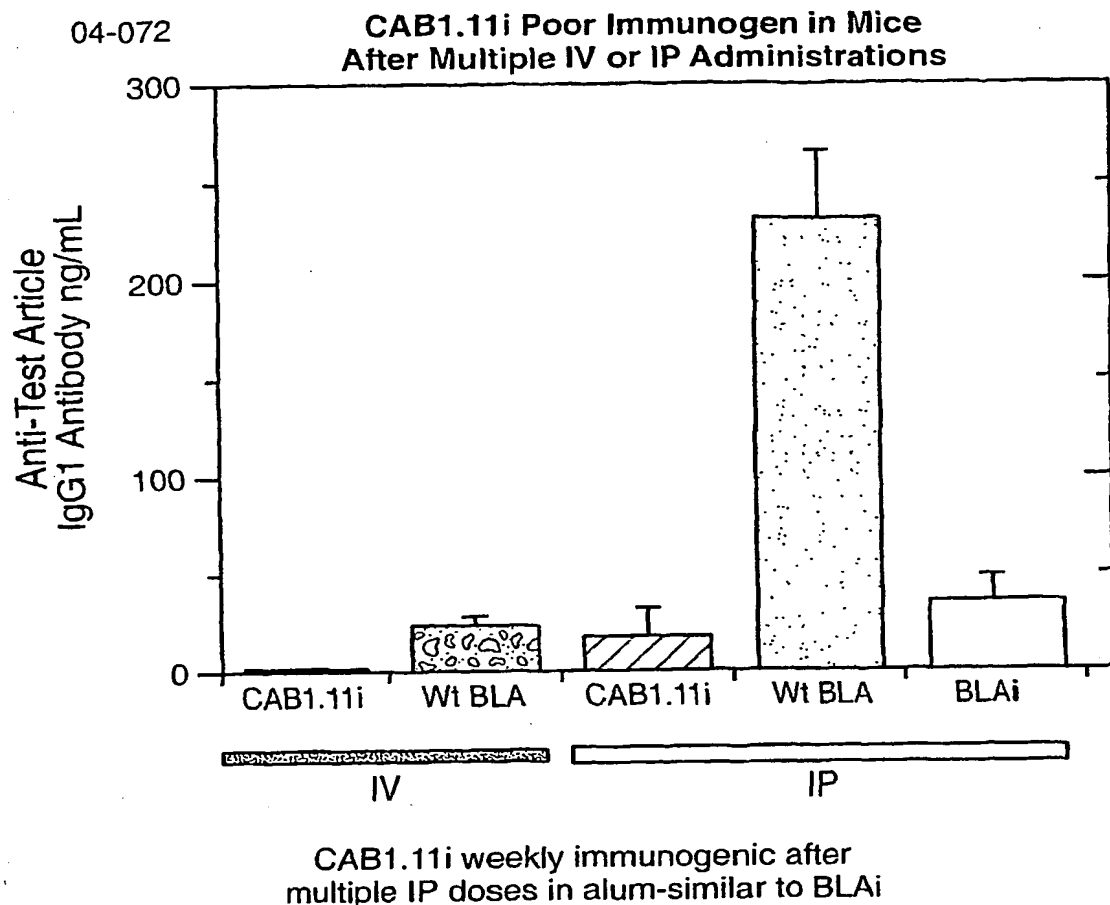
31 / 39

**FIG. 19A**

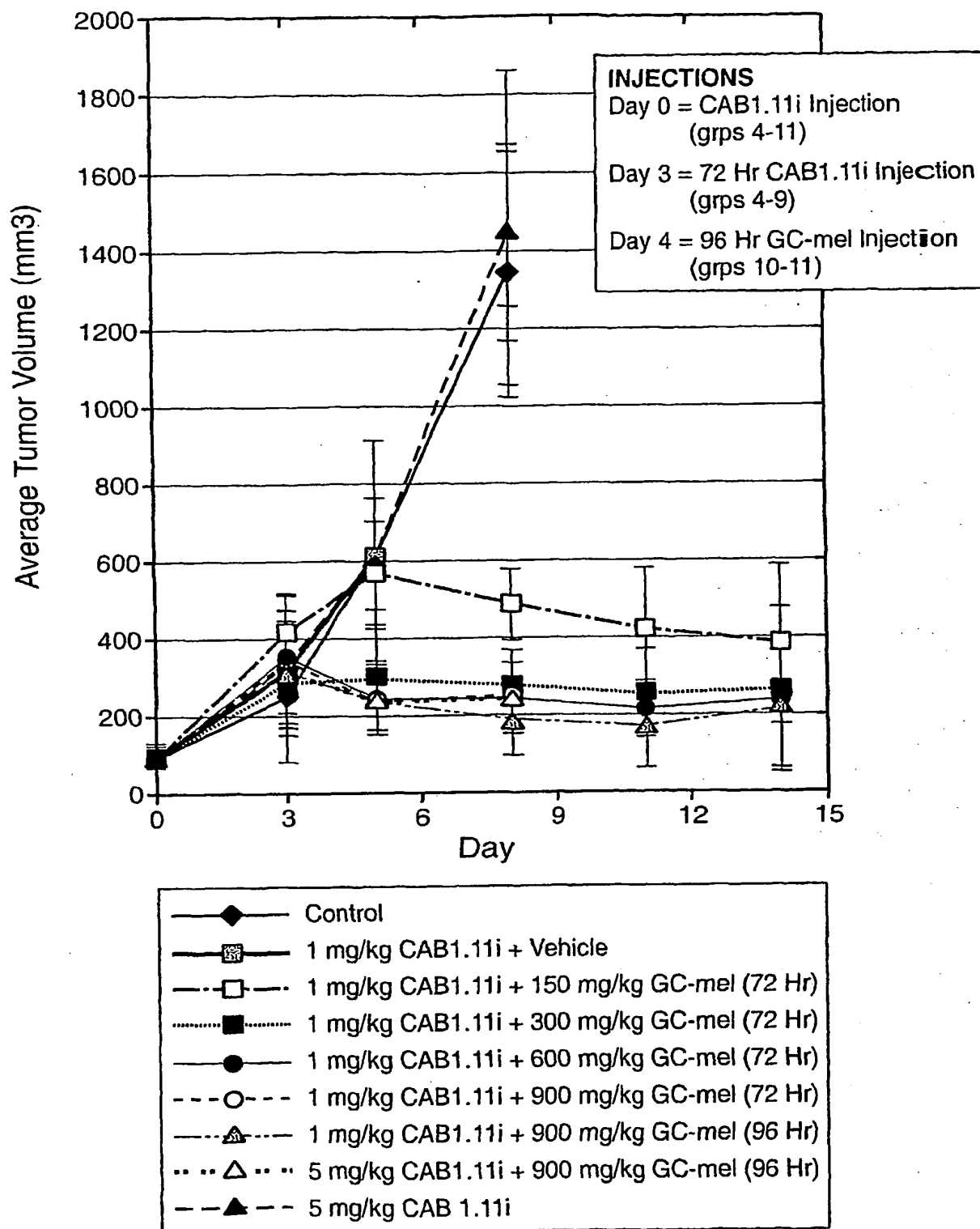
04-066 Completed

**FIG. 19B**

32 / 39

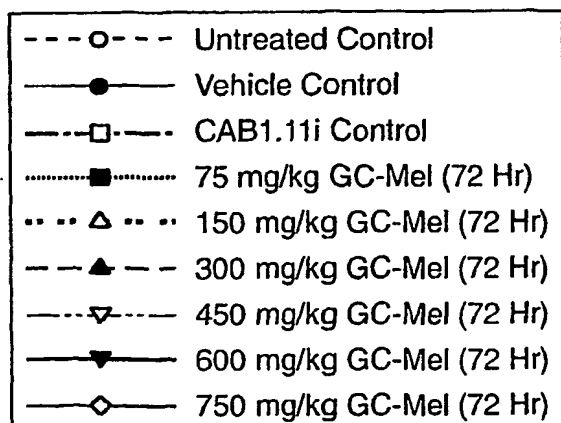
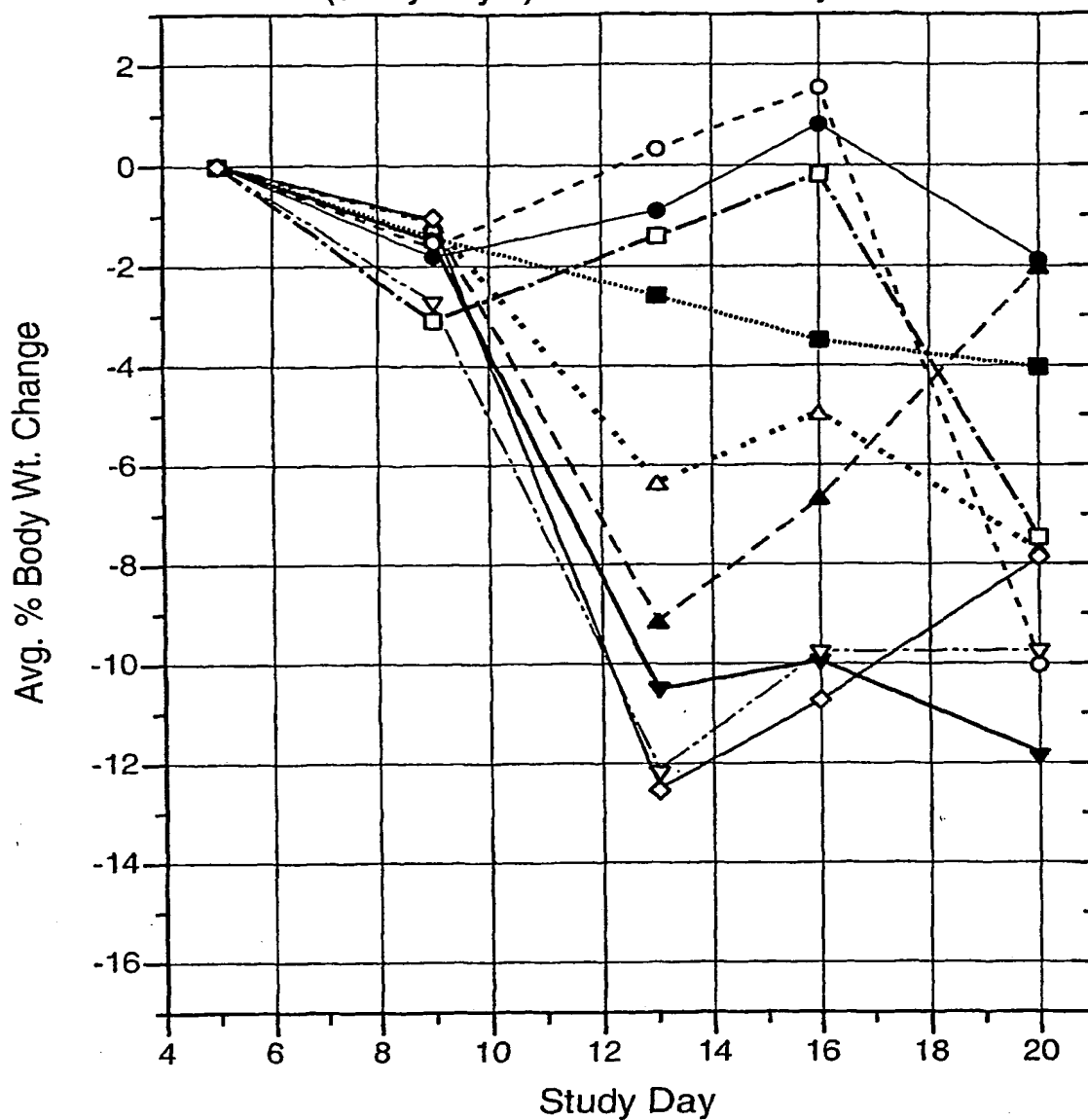
**FIG. 20**

33 / 39

**FIG. 21**

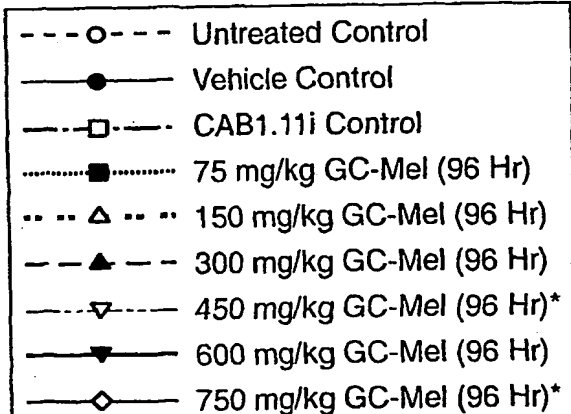
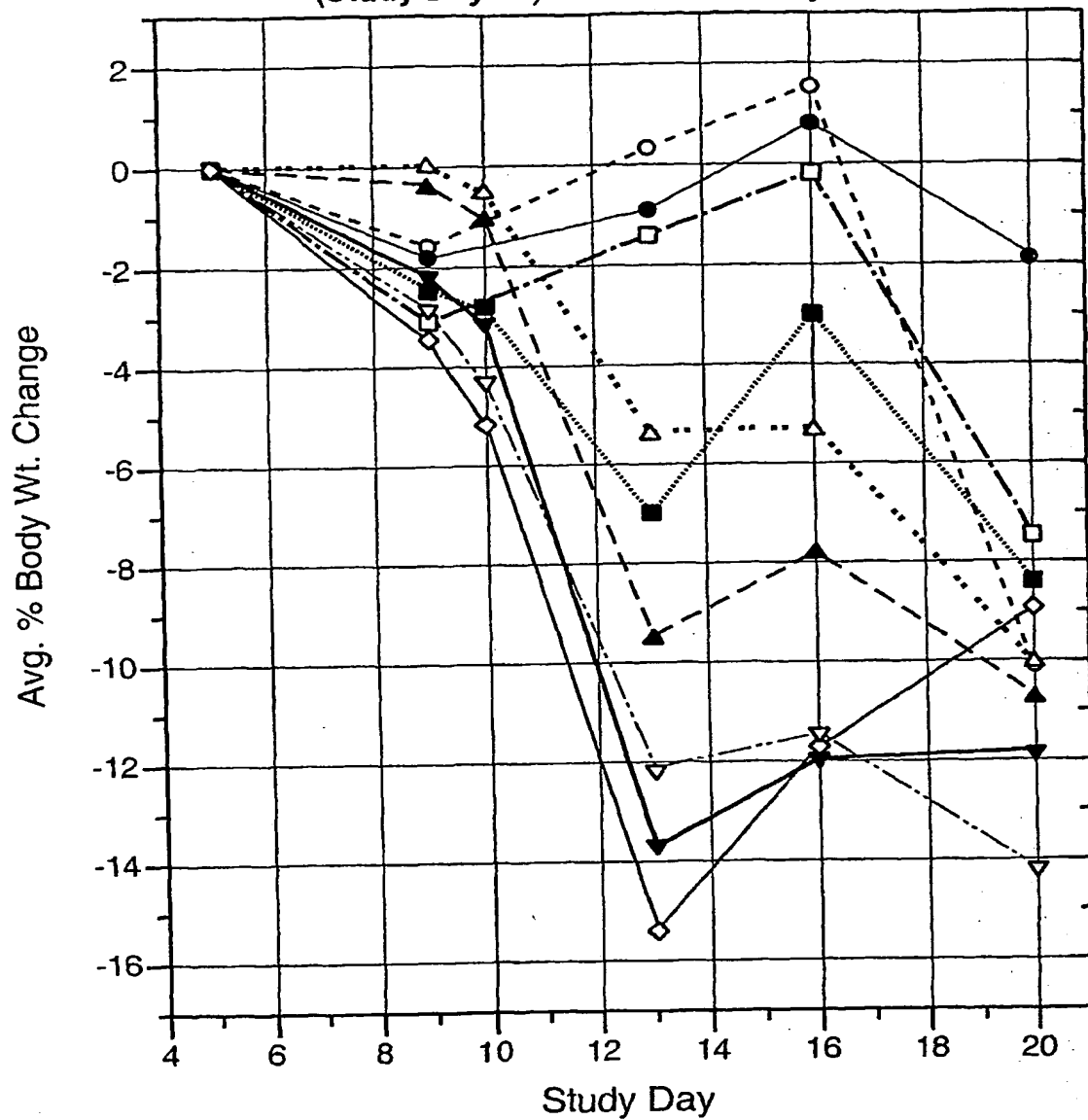
34 / 39

Avg. % Body Wt. Loss – GC-mel Injection 72 Hrs.
(Study Day 9) Post GCR-8886 Injection

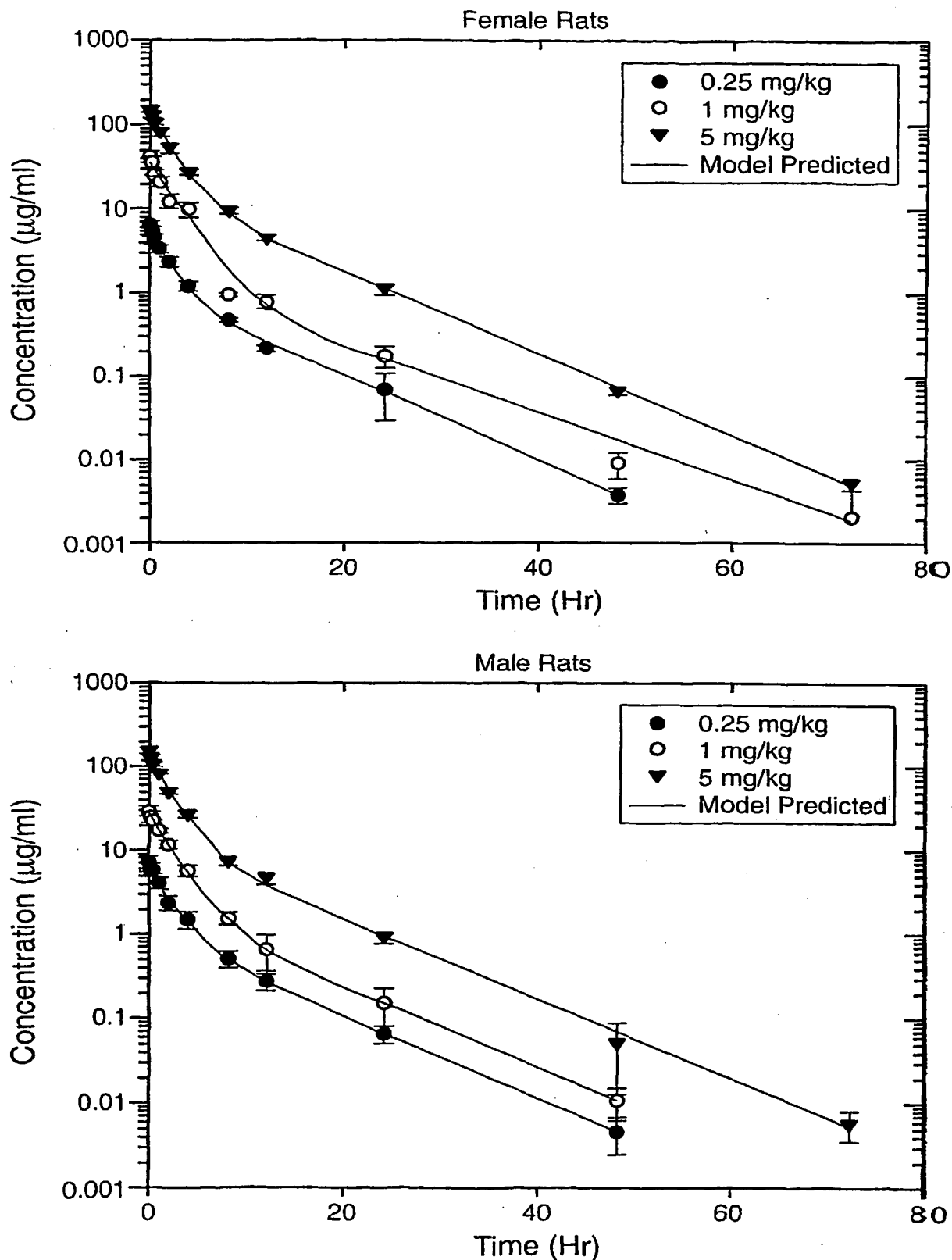
**FIG. 22A**

35 / 39

Avg. % Body Wt. Loss – GC-mel Injection 96 Hrs.
(Study Day 10) Post CAB1.11i Injection

**FIG. 22B**

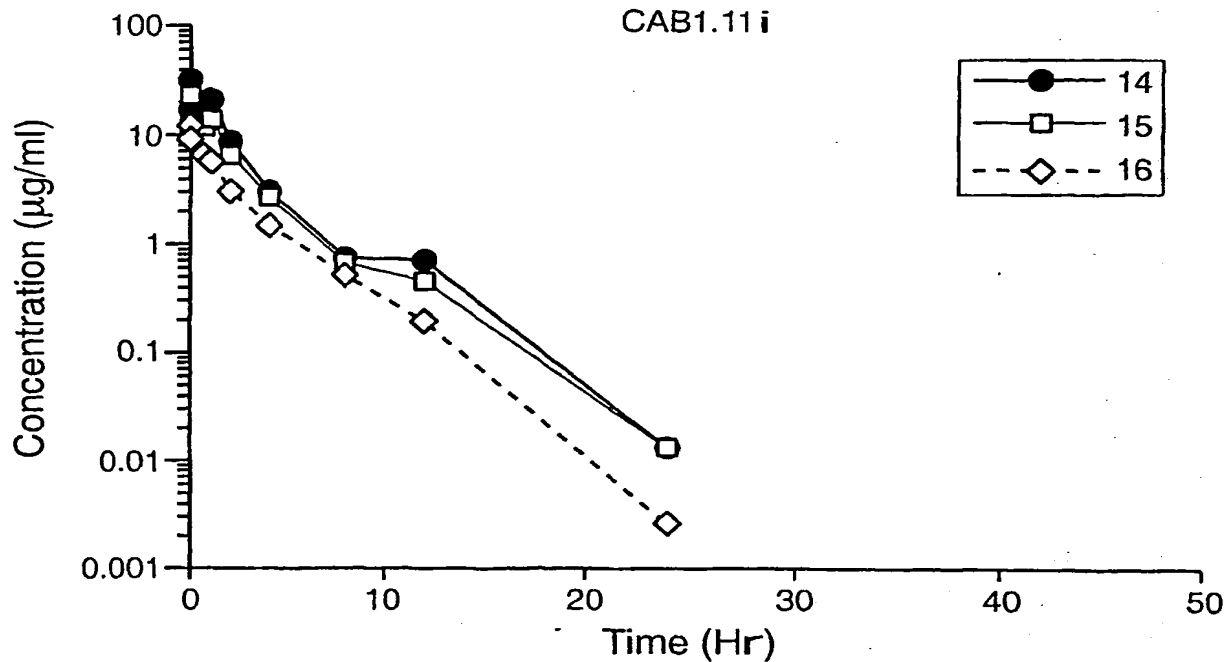
36 / 39

**Plasma CAB1.11i Concentration-time Profile in Rats
Results****FIG. 23**

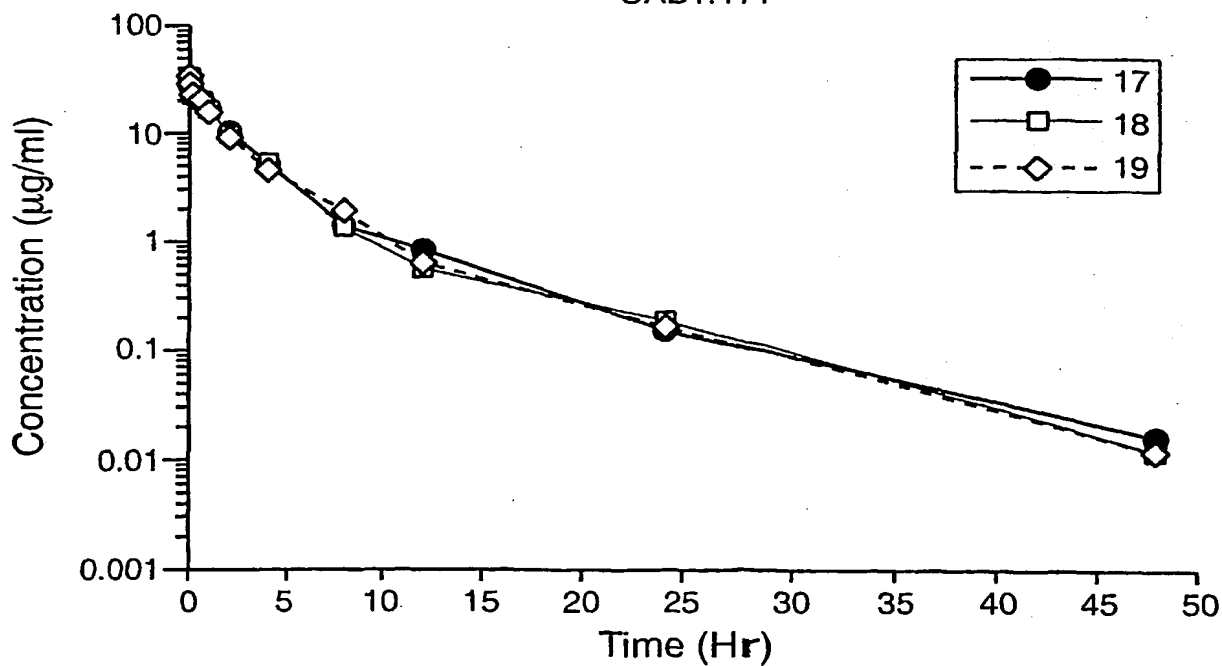
37 / 39

Plasma GCR-8886 Concentration-time Profiles in Rats
Results

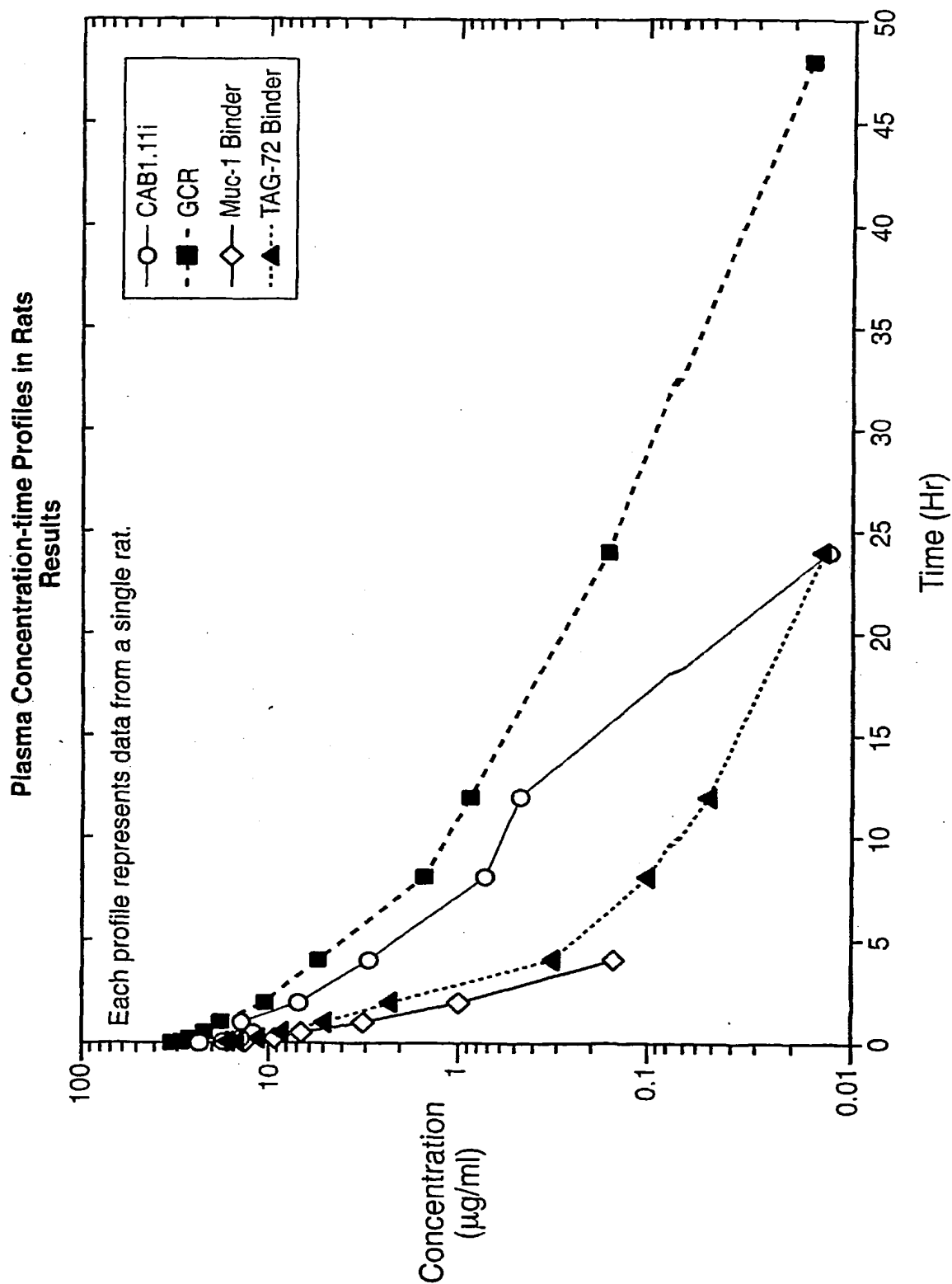
CAB1.11 i



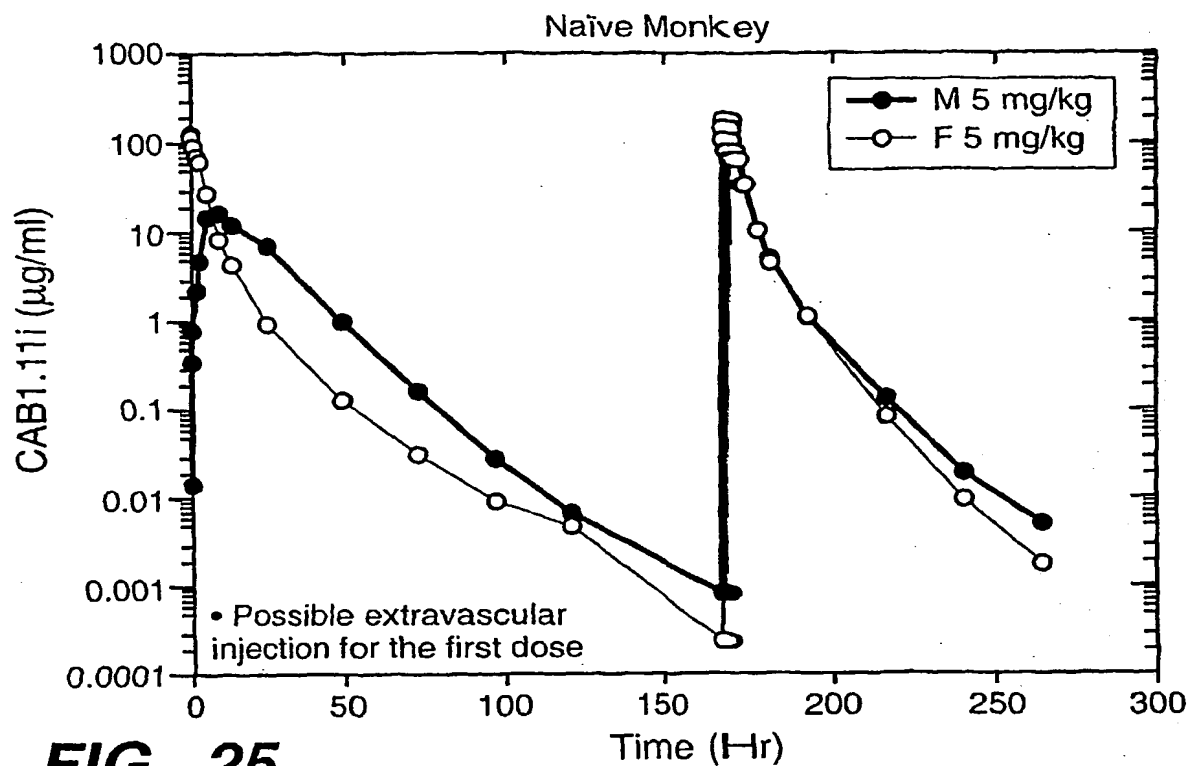
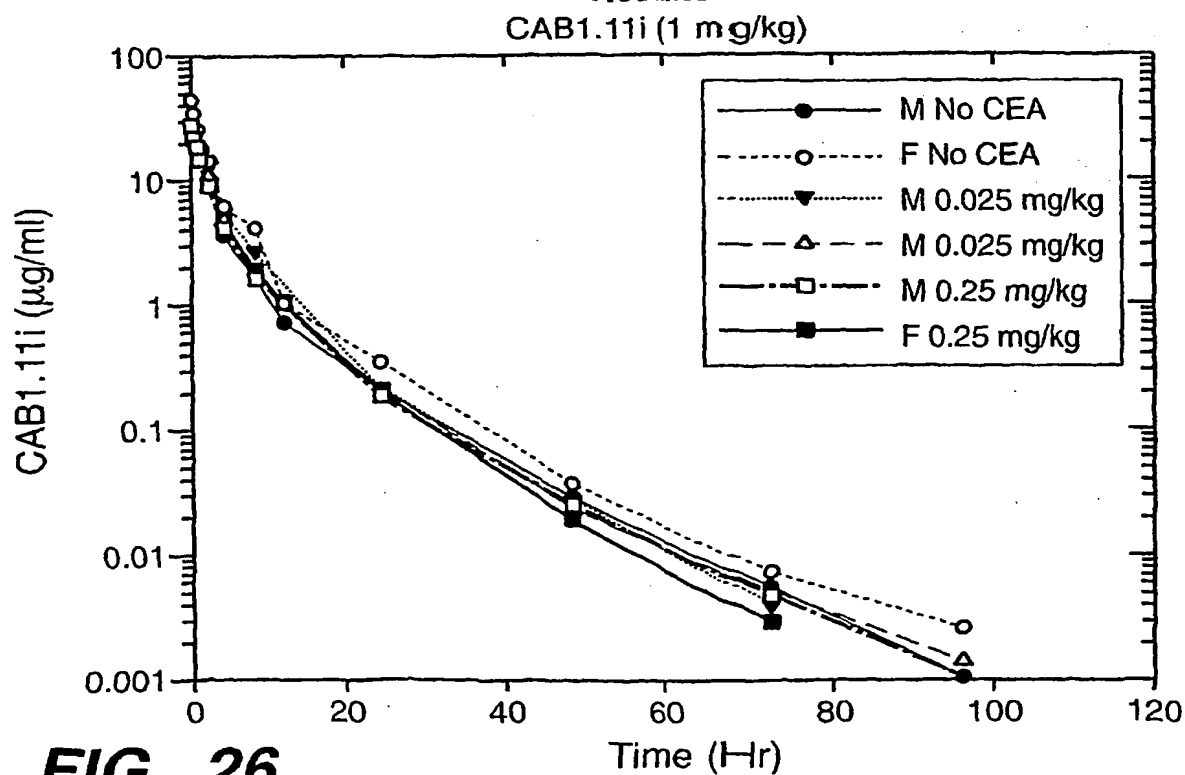
CAB1.11 i

**FIG. 24A**

38 / 39

**FIG. 24B**

39 / 39

**GCR-8886 Concentration-time Profiles Following 2 Weekly Doses
Results****FIG. 25****CAB1.11i PK Parameter Estimates with or without CEA Coadministration
Results****FIG. 26**

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.